

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 13:07:03 ; Search time 100.009 Seconds
(without alignments)
2909.975 Million cell updates/sec

Title: US-09-856-681A-2

Perfect score: 5450

Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	5450	100.0	1030	3	AAY71460	Aay71460 Human sem
2	5371.5	98.6	1047	6	ADA23362	Ada23362 Human SEC
3	5103.5	93.6	975	4	AAB90731	Aab90731 Human CJ1
4	5088	93.4	974	2	AAW64221	Aaw64221 Human sec
5	4921	90.3	939	3	AAB23030	Aab23030 Human sem
6	4921	90.3	939	6	ADA23281	Ada23281 Human SEC
7	4590.5	84.2	884	3	AAB23031	Aab23031 Human sem
8	4590.5	84.2	884	6	ADA23283	Ada23283 Human SEC
9	3677	67.5	699	4	AAB95139	Aab95139 Human pro

10	3373	61.9	630	3	AAB23043	Aab23043 Human sem
11	3373	61.9	630	6	ADA23307	Ada23307 Human SEC
12	3362	61.7	626	6	ADA23360	Ada23360 Human SEC
13	2980.5	54.7	574	4	AAB95317	Aab95317 Human pro
14	2952	54.2	562	4	AAB94104	Aab94104 Human pro
15	2947	54.1	562	4	AAM93444	Aam93444 Human pol
16	2891	53.0	863	4	ABG04066	Abg04066 Novel hum
17	2879.5	52.8	962	4	ABG04620	Abg04620 Novel hum
18	2621.5	48.1	507	4	AAB92688	Aab92688 Human pro
19	2361.5	43.3	1086	4	AAG63213	Aag63213 Amino aci
20	2349.5	43.1	1088	5	ABG79177	Abg79177 Human sem
21	2346	43.0	1017	5	AAG79413	Aag79413 CADHP-2,
22	2335	42.8	1035	5	ABG79173	Abg79173 Human sem
23	2326.5	42.7	1032	5	ABG79175	Abg79175 Human sem
24	2213	40.6	418	4	AAB95886	Aab95886 Human pro
25	2013.5	36.9	888	2	AAW19857	Aaw19857 Human sem
26	2009.5	36.9	888	3	AAB18916	Aab18916 A novel p
27	2009.5	36.9	888	4	AAU12443	Aau12443 Human PRO
28	2009.5	36.9	888	5	ABB84950	Abb84950 Human PRO
29	2009.5	36.9	888	5	ABB95556	Abb95556 Human ang
30	2009.5	36.9	888	6	ABO17887	Abo17887 Novel hum
31	2009.5	36.9	888	6	ABU69110	Abu69110 Human PRO
32	2009.5	36.9	888	6	ABU81141	Abu81141 Human PRO
33	2009.5	36.9	888	6	ABO19426	Abo19426 Human sec
34	2009.5	36.9	888	6	ABU66841	Abu66841 Human PRO
35	2009.5	36.9	888	6	ABU59922	Abu59922 Novel sec
36	2009.5	36.9	888	6	ABU69087	Abu69087 Human PRO
37	2009.5	36.9	888	6	ABO25112	Abo25112 Human sec
38	2009.5	36.9	888	6	ABU67117	Abu67117 Human sec
39	2009.5	36.9	888	6	ABU81551	Abu81551 Human sec
40	2009.5	36.9	888	6	ADA46063	Ada46063 Novel hum
41	2009.5	36.9	888	6	ADA76560	Ada76560 Novel hum
42	2009.5	36.9	888	6	ADA76494	Ada76494 Human PRO
43	2009.5	36.9	888	6	ADA19144	Ada19144 Human PRO
44	2009.5	36.9	888	6	ADA61767	Ada61767 Homo sapi
45	2009.5	36.9	888	6	ADB19552	Adb19552 Novel hum

ALIGNMENTS

RESULT 1
 AAY71460
 ID AAY71460 standard; protein; 1030 AA.
 XX
 AC AAY71460;
 XX
 DT 04-OCT-2000 (first entry)
 XX
 DE Human semaphorin 6A-1.
 XX
 KW Human; semaphorin 6A-1; (HSA) SEMA6A-1; neuronal development; apoptosis;
 KW neuronal regeneration; Ena/VASP protein family; immunomodulatory;
 KW gene therapy; diagnostic agent; therapeutic agent; differentiation;
 KW cytoskeletal stabilisation; plasticity.
 XX
 OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Binding-site 957. .961
FT /note= "Specific binding motif for members of Ena/VASP protein family, especially Evl"
FT Binding-site 959. .1030
FT /note= "Zyxin-like domain that selectively binds to members of Ena/VASP protein family, especially Evl"
FT Binding-site 1009. .1014
FT /note= "Specific binding motif for members of Ena/VASP protein family, especially Evl"
XX
PN WO200031252-A1.
XX
PD 02-JUN-2000.
XX
PF 26-NOV-1999; 99WO-EP009215.
XX
PR 26-NOV-1998; 98EP-00122441.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Behl C, Klostermann A;
XX
DR WPI; 2000-400065/34.
DR N-PSDB; AAD01233.
XX
PT Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent,
PT therapeutic agent, for modulating immune system, in gene therapy or for
PT effecting differentiation, cytoskeletal stabilization and/or plasticity.
XX
PS Example 1; Page 29-33; 53pp; English.
XX
CC The present sequence is a transmembranous human semaphorin 6A-1
CC ((HSA)SEMA6A-1) which is involved in neuronal development and
CC regeneration mechanisms during apoptosis. Semaphorin is a family of
CC proteins displaying secreted or transmembrane-based repulsive guidance
CC cues critically involved in neuronal development. The present sequence
CC was isolated from human 1-ZAP Express cDNA library which was screened
CC using a PCR fragment amplified from human neuroblastoma cell line SK-N-MC
CC cDNA. The (HSA)SEMA6A-1 protein contains a Zyxin-like domain that
CC selectively binds to members of Ena/VASP protein family especially Evl.
CC Expression of (HSA)SEMA6A-1 is highest in embryonic brain and kidney and
CC moderate in lung. The present sequence is useful as diagnostic and
CC therapeutic agents, for modulating the immune system, in gene therapy,
CC for effecting differentiation, cytoskeletal stabilisation and plasticity
XX
SQ Sequence 1030 AA;

Query Match 100.0%; Score 5450; DB 3; Length 1030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPISHGNYTKQYPVFVGHKPGNNTTQRHRLDIQM 60
|||
Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPISHGNYTKQYPVFVGHKPGNNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120
|||
Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120

Qy 121 IKVLLKKNDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCYPYDAKHANVALFADG 180
|||
Db 121 IKVLLKKNDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCYPYDAKHANVALFADG 180

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
|||
Db 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy 241 VEYNTMGKVVFPRVAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
|||
Db 241 VEYNTMGKVVFPRVAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
|||
Db 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
|||
Db 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKSYD 480
|||
Db 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKSYD 480

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRERHGKCKKTCIASRDPYCGWIKEGG 540
|||
Db 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRERHGKCKKTCIASRDPYCGWIKEGG 540

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESR 600
|||
Db 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESR 600

Qy 601 GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLGHDQLPVTLIAAVILAFV 660
|||
Db 601 GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLGHDQLPVTLIAAVILAFV 660

Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGLFGDTQSKDPKPE 720
|||
Db 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGLFGDTQSKDPKPE 720

Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGREWERN 780
|||
Db 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGREWERN 780

Qy 781 QNLINACTKDMPPMGSPIPTDPLRASPISHIPSVVVLPIQQGYQHEYVDQPKMSEVAQ 840
|||
Db 781 QNLINACTKDMPPMGSPIPTDPLRASPISHIPSVVVLPIQQGYQHEYVDQPKMSEVAQ 840

Qy 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
|||
Db 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900

Qy 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLSRNQSFGRGDNPP 960

Db ||||||| 901 SKRLEMHHSSSYGVDYKRSYPTNSLRSHQATTLKRNNTNSSNSHLSRNQSFGRGDNPP 960
Qy 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS 1020
Db ||||||| 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS 1020
Qy 1021 TSMKPNDACT 1030
Db ||||||| 1021 TSMKPNDACT 1030

RESULT 2

ADA23362

ID ADA23362 standard; protein; 1047 AA.

XX

AC ADA23362;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide, SEC15.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
KW cardiovascular disease; oncology disease; immune disorder;
KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological.

XX

OS Homo sapiens.

XX

PN US2003054514-A1.

XX

PD 20-MAR-2003.

XX

PF 19-SEP-2001; 2001US-00957187.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 04-JAN-2000; 2000US-0174485P.

PR 08-MAR-2000; 2000US-00520781.

PR 19-SEP-2000; 2000US-0233798P.

PR 20-SEP-2000; 2000US-0234082P.

XX

PA (SHIM/) SHIMKETS R A.

PA (LARO/) LAROCHELLE W J.

XX

PI Shimkets RA, Larochele WJ;

XX

DR WPI; 2003-540616/51.

DR N-PSDB; ADA23361.

XX

PT New SECX nucleic acids, useful for treating or diagnosing a disorder

PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder, and autoimmune disease.

XX

PS Claim 12; Page 14; 118pp; English.

XX

CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence represents a
CC polypeptide of the invention.

XX

SQ Sequence 1047 AA;

Query Match 98.6%; Score 5371.5; DB 6; Length 1047;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1023; Conservative 0; Mismatches 7; Indels 17; Gaps 1;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHCNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKLTWKSQADVDTCRMKGKHKDECHNF 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKLTWKSQADVDTCRMKGKHKDECHNF 120

Qy 121 IKVLLKKNDDALFVCGTNAFN PSCRNYKMDTLEPGDEFSGMARC PYDAKHANVALFADG 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 IKVLLKKNDDALFVCGTNAFN PSCRNYKMDTLEPGDEFSGMARC PYDAKHANVALFADG 180

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHD SKWLKEPYFVQAVDYGDIYFFFREIA 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHD SKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy 241 VEYNTMGKVV FPRVAQVCKNDMGGSQ RVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 VEYNTMGKVV FPRVAQVCKNDMGGSQ RVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGS AVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 DVIRINGRDVVLATFSTPYNSIPGS AVCAYDMLDIASVGTGRFKEQKSPDSTWTPVPDER 360

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKG IILKFLARIGNSGFLNDSL FLEEMSVN SEKCSYD 480
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 421 TKIAVDTAAGPYQNHTVVFLGSEKG IILKFLARIGNSGFLNDSL FLEEMSVN SEKCSYD 480

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHGKCKTCIAS RD PYCGWIKEGG 540

Db	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKBPLGRDERHGKCKKTCIASRDPYCGWIKEGG	540
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	583
Db	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSLL	600
Qy	584	PSTTTSDSTAQEYESRGGM DWKHLLDPDSTDPLGAVSSHNNHQDKKGVIRESYLGHD	643
Db	601	PSTTTSDSTAQEYESRGGM DWKHLLDPDSTDPLGAVSSHNNHQDKKGVIRESYLGHD	660
Qy	644	QLVPVTLLAIAVILAFVMGA VFSGITVYCVCDHRRKDVA VQRKEKELTHSRRGSMSSVT	703
Db	661	QLVPVTLLAIAVILAFVMGA VFSGITVYCVCDHRRKDVA VQRKEKELTHSRRGSMSSVT	720
Qy	704	KLSGLFGDTQS KDPKPEA ILTPLMHNGKLATPGNTAKMLI KADQHHLDLTALPTPESTPT	763
Db	721	KLSGLFGDTWS KDPKPEA ILTPLMHNGKLATPGNTAKMLI KADQHHLDLTALPTPESTPT	780
Qy	764	LQQKRKP SRGSREWERNQN LINACTKDMPPMGSPV IPTDLPLRASP SHIPS VVVL PITQQ	823
Db	781	LQQKRKP SRGSREWERNQN LINACTKDMPPMGSPV IPTCLPLRASP SHIPS VVVL PITQQ	840
Qy	824	GYQHEYVDQPKMSEVAQMALE DQAATLEYKTIKEHLSSKSPN HGVNLVENLDSL PPKV PQ	883
Db	841	BYQHEYVDQPKMSEVAQMALE DQAATLEYKTIKEHLSSKSPN HGVNLVENLDSL PPKV PQ	900
Qy	884	REASLGPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATT LKRNNNTNSSN	943
Db	901	REASLGPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATT LKRNNNTNSSN	960
Qy	944	SSHLSRNQSFGRGDNP PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYN SLTRSGLKRT	1003
Db	961	SSHLSRNQSFGRGDNP PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYN SLTRSGLKRT	1020
Qy	1004	PSLKPDVPPKPSFAPLSTS MKPND ACT	1030
Db	1021	PSLKPDVPPKPSFAPLSTS MKPND ACT	1047

RESULT 3

AAB90731

ID AAB90731 standard; protein; 975 AA.

xx

AC AAB90731;

xx

DT 07-JUN-2001 (first entry)

xx

DE Human CJ145_1 protein sequence SEQ ID 161.

xx

KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
KW differentiation; immune system modulator; tissue growth; chemotactic;
KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
KW haematopoiesis.

xx

OS *Homo sapiens.*

xx

PN WO200119988-A1.

XX

PD 22-MAR-2001.

XX

PF 14-SEP-2000; 2000WO-US025135.

XX

PR 17-SEP-1999; 99US-00398829.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;

XX

DR WPI; 2001-244801/25.

DR N-PSDB; AAF98469.

XX

PT Isolated nucleic acids encoding polypeptides, useful for modulating e.g.
PT cytokine and cell proliferation/differentiation activity, the immune
PT system and hematopoiesis regulating activity.

XX

PS Disclosure; Page 487-490; 557pp; English.

XX

CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
CC tissue types, and may be used in the prevention, treatment and diagnosis
CC of diseases associated with inappropriate protein expression. The
CC polypeptides and nucleic acids may be used as nutrients or to modulate
CC cytokine and cell proliferation/differentiation activity and may also be
CC involved in modulation of the immune system. The cDNA sequences,
CC proteins, their agonists and/or antagonists exhibit haematopoiesis
CC regulating activity; tissue growth activity; activin/inhibin activity;
CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;
CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis
CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition
CC activity. Included in the invention are probes represented in AAF98490 -
CC AAF98572 which are specific for the cDNA clones encoding the secreted
CC proteins

XX

SQ Sequence 975 AA;

Query Match 93.6%; Score 5103.5; DB 4; Length 975;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 972; Conservative 0; Mismatches 3; Indels 55; Gaps 1;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHDECHNF 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHDECHNF 120

Qy 121 IKVLLKKNDALFVCGTNAFN PSCRNYKMDTLEPFGDEFSGMARC PYDAKHANVALFADG 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 IKVLLKKNDALFVCGTNAFN PSCRNYKMDTLEPFGDEFSGMARC PYDAKHANVALFADG 180

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240

Db ||||||| 181 KLYSATVTDLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy 241 VEYNTMGKVVFPRVAQVCKNDMGGSVRLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
||| 241 VEYNTMGKVVFPRVAQVCKNDMGGSVRLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
||| 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
||| 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD 480
||| 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD 480

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 540
||| 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 540

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESR 600
||| 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN----- 576

Qy 601 GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLQLPVTLLAIAVILAFV 660
||| 577 -----GVIRESYLKGHDLQLPVTLLAIAVILAFV 605

Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSVTKLSGLFGDTQSKDPKPE 720
||| 606 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSVTKLSGLFGDTQSKDPKPE 665

Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSRREWERN 780
||| 666 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSRREWERN 725

Qy 781 QNLINACTKDMPPMGSPVIPTDPLRASPISHIPSVVVLPIQQGYQHEYVDQPKMSEVAQ 840
||| 726 QNLINACTKDMPPMGSPVIPTDPLRASPISHIPSVVVLPIQQGYQHEYVDQPKMSEVAQ 785

Qy 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
||| 786 MALEDQAATLEYKTIKEHFSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLFQTGL 845

Qy 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLSRNQSFGRGDNPP 960
||| 846 SKRLEMHHSFSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLSRNQSFGRGDNPP 905

Qy 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLRSGLKRTPSLKPDPVPPKPSFAPLS 1020
||| 906 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLRSGLKRTPSLKPDPVPPKPSFAPLS 965

Qy 1021 TSMKPNDACT 1030
|||

RESULT 4

AAW64221

ID AAW64221 standard; protein; 974 AA.

XX

AC AAW64221;

XX

DT 06-OCT-1998 (first entry)

XX

DE Human secreted protein from clone CJ145_1.

XX

KW Secreted protein; human fetal brain; nutrition; cytokine; stimulant;
KW cell proliferation; differentiation; immune system; suppressor; ligand;
KW regulator; hematopoiesis; tissue growth; activin; inhibin; haemostatic;
KW chemotaxis; chemokinetic; thrombosis; receptor; cadherin; tumour;
KW anti-inflammatory.

XX

OS Homo sapiens.

XX

PN WO9827205-A2.

XX

PD 25-JUN-1998.

XX

PF 17-DEC-1997; 97WO-US023330.

XX

PR 18-DEC-1996; 96US-00769192.

PR 13-JAN-1997; 97US-00783401.

PR 16-DEC-1997; 97US-00991872.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

PI Spaulding V, Agostino MJ;

XX

DR WPI; 1998-362774/31.

DR N-PSDB; AAV44295.

XX

PT New polynucleotides and secreted proteins - obtained from human foetal
PT brain, human adult testes, human adult brain and human adult salivary
PT gland cDNA libraries.

XX

PS Claim 17j; Page 71-74; 110pp; English.

XX

CC This sequence represents a novel secreted protein from clone CJ145_1
CC isolated from a human fetal brain cDNA library. This protein has
CC applications for nutritional use, cytokine and cell
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, hematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombotic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity and other activities

XX

SQ Sequence 974 AA;

Query Match 93.4%; Score 5088; DB 2; Length 974;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 971; Conservative 0; Mismatches 3; Indels 56; Gaps 2;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPFVGHKPGRNTTQRHRLDIQM 60
Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVIDTSHTEEIYCSKKLTWKSQADVDTCRMKGHKDECHNF 120
Db 61 IMIMNGTLYIAARDHIYTVIDTSH-EEIYCSKKLTWKSQADVDTCRMKGHKDECHNF 119

Qy 121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPFGDESGMARCPYDAKHANVALFADG 180
Db 120 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPFGDESGMARCPYDAKHANVALFADG 179

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
Db 180 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 239

Qy 241 VEYNTMGKVVFPRAQVCKNDMGGSSQRLKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
Db 240 VEYNTMGKVVFPRAQVCKNDMGGSSQRLKQWTSFLKARLNCSVPGDSHFYFNILQAVT 299

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSACAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
Db 300 DVIRINGRDVVLATFSTPYNSIPGSACAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 359

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
Db 360 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 419

Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNSEKSYD 480
Db 420 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNSEKSYD 479

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKKTCIASRDPYCGWIKEGG 540
Db 480 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKKTCIASRDPYCGWIKEGG 539

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQEYESR 600
Db 540 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN----- 575

Qy 601 GGMLDWKHLLDSPSTDPLGAVSSHNHQDKKGVIRESYLKGHDQLVPVTLLAIAVILAFV 660
Db 576 -----GVIRESYLKGHDLQVPTLLAIAVILAFV 604

Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSVTKLSQLFGDTQSKDPKPE 720
Db 605 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSVTKLSQLFGDTQSKDPKPE 664

Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGREWERN 780
Db 665 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGREWERN 724

Qy 781 QNLINACTKDMPPMGS PVIPTDPLRASPSHIPS VVLPITQQGYQHEYVDQP KMS EVAQ 840

Db ||||||| 725 QNLINACTKDMPPMGSPVIPTDLPLRASPISHPSVVVLPIQQGYQHEYVDQPKMSEVAQ 784
Qy 841 MALEDQAATLEYKTIKEHLSSKSPNHGVLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
Db ||||||| 785 MALEDQAATLEYKTIKEHFSSKSPNHGVLVENLDSLPPKVPQREASLGPPGASLFQTGL 844
Qy 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSSLRNQSFGRGDNPP 960
Db ||||||| 845 SKRLEMHHSFSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSSLRNQSFGRGDNPP 904
Qy 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS 1020
Db ||||||| 905 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPLS 964
Qy 1021 TSMKPNDACT 1030
Db ||||||| 965 TSMKPNDACT 974

RESULT 5

AAB23030

ID AAB23030 standard; protein; 939 AA.

XX

AC AAB23030;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant, SECX 2864933-1.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200053742-A2.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US006280.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-0520781P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA;

XX

DR WPI; 2000-594318/56.

DR N-PSDB; AAA93617.

XX

PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.

XX

PS Claim 1; Fig 2; 151pp; English.

XX

CC Sequences AAB23029-B23048 represent human SECX proteins. The SECX
CC proteins of the invention are either secreted or membrane-associated
CC proteins and act as regulator of cellular proliferation and
CC differentiation. SECX proteins or nucleotides are useful for diagnosing
CC the presence of, or predisposition to, a disease associated with altered
CC levels of SECX proteins and nucleotides. The SECX proteins are also
CC useful to screen compounds that modulate SECX activity or expression. The
CC interaction of a SECX protein with other cellular proteins may be useful
CC to modulate the activity of a partner protein, cellular proliferation,
CC cellular differentiation and cell survival. SECX nucleotides are useful
CC for the recombinant expression of SECX protein, and may be used detect
CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to
CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX
CC nucleic acid sequences are also useful for identifying a cell or tissue
CC type in a biological sample, and in forensic biology. SECX primers or
CC probes are useful for detecting the presence of SECX nucleotides and for
CC screening tissue cultures for contamination. Diseases that may be treated
CC or prevented using SECX proteins or nucleotides include cancer (e.g.,
CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
CC or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 939 AA;

Query Match 90.3%; Score 4921; DB 3; Length 939;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 928; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGHKDECHNF 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGHKDECHNF 120

Qy 121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPFGDEFSGMARCYDAKHANVALFADG 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPFGDEFSGMARCYDAKHANVALFADG 180

Qy 181 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240

Qy 241 VEYNTMGKVVFPRVAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Db	241 VEYNTMGKVVPRVAQVKNDMGGSQRVLEKQWTSFLKARLNCSVPGDHFYFNILQAVT 300
Qy	301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
Db	301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
Qy	361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
Db	361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
Qy	421 TKIAVDTAAGPYQNHTVVFGLSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD 480
Db	421 TKIAVDTAAGPYQNHTVVFGLSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD 480
Qy	481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGCKKTCIASRDPYCGWIKEGG 540
Db	481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGCKKTCIASRDPYCGWIKEGG 540
Qy	541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQEYESR 600
Db	541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQEYESR 600
Qy	601 GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLQLPVTLLAIAVILA 660
Db	601 GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLQLPVTLLAIAVILA 660
Qy	661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGLFGDTQS KDPKPE 720
Db	661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGLFGDTQS KDPKPE 720
Qy	721 AILTPLMHNGKLATPGNTAKMLIKADQHLDLTALPTPESTPTLQQKRKPSRGSRGSREWERN 780 : :
Db	721 AILTPLMHNGKLATPGNTAKMLIKADQHLDLTALPTPESTPTLQQKRKPSRGSRGSREWERN 780
Qy	781 QNLINACTKDMPPMGS PVIPTDLPLRASP SHIPS VVVL PITQQGYQHEYVDQPKMSEVAQ 840
Db	781 QNLINACTKDMPPMGS PVIPTDLPLRASP SHIPS VVVL PITQQGYQHEYVDQPKMSEVAQ 840
Qy	841 MALEDQAATLEYKTIKEHLSKSPN HGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
Db	841 MALEDQAATLEYKTIKEHLSKSPN HGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
Qy	901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQAT 932
Db	901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHLTT 932

RESULT 6

ADA23281
 ID ADA23281 standard; protein; 939 AA.
 XX
 AC ADA23281;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human SECX polypeptide, SEC2.

XX
KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
KW cardiovascular disease; oncology disease; immune disorder;
KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological.
XX
OS Homo sapiens.
XX
PN US2003054514-A1.
XX
PD 20-MAR-2003.
XX
PF 19-SEP-2001; 2001US-00957187.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
XX
PI Shimkets RA, Larochelele WJ;
XX
DR WPI; 2003-540616/51.
DR N-PSDB; ADA23280.
XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 12; Fig 2; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence represents a
CC SECX polypeptide of the invention.
XX
SQ Sequence 939 AA;

Query Match

90.3%; Score 4921; DB 6; Length 939;

Best Local Similarity 99.6%; Pred. No. 0;
Matches 928; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGHKDECHNF 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGHKDECHNF 120

Qy 121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCYPDAKHANVALFADG 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCYPDAKHANVALFADG 180

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy 241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 VEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVNSEKCSYD 480
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVNSEKCSYD 480

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKTCIASRDPYCGWIKEGG 540
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKTCIASRDPYCGWIKEGG 540

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQEYESR 600
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQEYESR 600

Qy 601 GGMLDWKHLLSPDSTDPLGAVSSHNNHQDKKGVIRESYLKGDQLVPVTLLAIAVILAFV 660
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 GGMLDWKHLLSPDSTDPLGAVSSHNNHQDKKGVIRESYLKGDQLVPVTLLAIAVILAFV 660

Qy 661 MGAVFSGITVYCVCDHRRKDVAVQRKEKELTHSRRGSMSSVTKLSQLFGDTQSKDPKPE 720
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 MGAVFSGITVYCVCDHRRKDVAVQRKEKELTHSRRGSMSSVTKLSQLFGDTQSKDPKPE 720

Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHLDLTALPTPESTPTLQQKRKPSRGREWERN 780
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : ||| : |||
Db 721 AILTPLMHNGKLATPGNTAKMLIKADQHLDLTALPTPESTPTLQQKRKPSRGREWERN 780

Qy 781 QNLINACTKDMPPMGSPIPTDLPLRASPISHIPSVVLPITQQGYQHEYVDQPKMSEVAQ 840
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 781 QNLINACTKDMPPMGSPIPTDLPLRASPShIPSVVVLPTQQGYQHEYVDQPKMSEVAQ 840
Qy 841 MALEDQAATLEYKTIKEHLSSKSPNFGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 841 MALEDQAATLEYKTIKEHLSSKSPNFGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
Qy 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQAT 932
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHLTT 932

RESULT 7

AAB23031

ID AAB23031 standard; protein; 884 AA.

XX

AC AAB23031;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant, SECX 2864933-2.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200053742-A2.

XX

PD 14-SEP-2000.

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PF 09-MAR-2000; 2000WO-US006280.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-0520781P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA;

XX

DR WPI; 2000-594318/56.

DR N-PSDB; AAA93618.

XX

PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.

XX

PS Claim 1; Fig 3; 151pp; English.

XX

CC Sequences AAB23029-B23048 represent human SECX proteins. The SECX proteins of the invention are either secreted or membrane-associated proteins and act as regulator of cellular proliferation and differentiation. SECX proteins or nucleotides are useful for diagnosing the presence of, or predisposition to, a disease associated with altered levels of SECX proteins and nucleotides. The SECX proteins are also useful to screen compounds that modulate SECX activity or expression. The interaction of a SECX protein with other cellular proteins may be useful to modulate the activity of a partner protein, cellular proliferation, cellular differentiation and cell survival. SECX nucleotides are useful for the recombinant expression of SECX protein, and may be used to detect SECX mRNA or genetic lesions in the SECX gene. They may also be used to modulate SECX expression (e.g., using antisense oligonucleotides). SECX nucleic acid sequences are also useful for identifying a cell or tissue type in a biological sample, and in forensic biology. SECX primers or probes are useful for detecting the presence of SECX nucleotides and for screening tissue cultures for contamination. Diseases that may be treated or prevented using SECX proteins or nucleotides include cancer (e.g., colorectal carcinoma, prostate cancer), benign tumours, immune disorders (including autoimmune diseases, transplant rejection, allergies, AIDS), infections, inflammatory disorders, arthritis, haematopoietic disorders, skin disorders, cardiovascular disorders, atherosclerosis, restenosis, neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 884 AA;

Query Match 84.2%; Score 4590.5; DB 3; Length 884;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 873; Conservative 2; Mismatches 2; Indels 55; Gaps 1;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
Db |||||||

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHDECHNF 120
Db |||||||

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHDECHNF 120

Qy 121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCPTYDAKHANVALFADG 180
Db |||||||

Qy 121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCPTYDAKHANVALFADG 180

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLEPYFVQAVDYGDIYFFREIA 240
Db |||||||

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLEPYFVQAVDYGDIYFFREIA 240

Qy 241 VEYNTMGKVVPRVAQVCKNDMGGSQLVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
Db |||||||

Qy 241 VEYNTMGKVVPRVAQVCKNDMGGSQLVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
Db |||||||

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMRYRL 420
Db |||||||

Db 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
 Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDLSLFLEEMSVNSEKCSYD 480
 |||||||
 Db 421 TKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDLSLFLEEMSVNSEKCSYD 480
 Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKTCIASRDPYCGWIKEGG 540
 |||||||
 Db 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKTCIASRDPYCGWIKEGG 540
 Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQEYESR 600
 |||||||
 Db 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN----- 576
 Qy 601 GGMLDWKHLLDSPDSTDPLGAVSSHNNQDKKGVIRESYLKGHDQLVPVTLLIAVILA 660
 |||||||
 Db 577 -----GVIRESYLKGHDQLVPVTLLIAVILA 605
 Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQS KDPKPE 720
 |||||||
 Db 606 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQS KDPKPE 665
 Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERN 780
 |||||||
 Db 666 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKREPSRGTRREWERN 725
 Qy 781 QNLINACTKDMPMGPSPVIPTDLPLRASPSPHI PSVVVLPI TQQGYQHEYVDQPKMSEVAQ 840
 |||||||
 Db 726 QNLINACTKDMPMGPSPVIPTDLPLRASPSPHI PSVVVLPI TQQGYQHEYVDQPKMSEVAQ 785
 Qy 841 MALEDQAATLEYKTIKEH LSSKSPN HGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
 |||||||
 Db 786 MALEDQAATLEYKTIKEH LSSKSPN HGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 845
 Qy 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQAT 932
 |||||||
 Db 846 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHLTT 877

RESULT 8

ADA23283

ID ADA23283 standard; protein; 884 AA.

XX

AC ADA23283;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide, SEC3 #1.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
 KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
 KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
 KW cardiovascular disease; oncology disease; immune disorder;
 KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
 KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
 KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
 KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological.
XX
OS Homo sapiens.
XX
PN US2003054514-A1.
XX
PD 20-MAR-2003.
XX
PF 19-SEP-2001; 2001US-00957187.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (SHIM//) SHIMKETS R A.
PA (LARO//) LAROCHELLE W J.
XX
PI Shimkets RA, Larochelle WJ;
XX
DR WPI; 2003-540616/51.
DR N-PSDB; ADA23282.
XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 12; Fig 3; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence represents a
CC SECX polypeptide of the invention.
XX
SQ Sequence 884 AA;

Query Match 84.2%; Score 4590.5; DB 6; Length 884;
 Best Local Similarity 93.7%; Pred. No. 0;
 Matches 873; Conservative 2; Mismatches 2; Indels 55; Gaps 1;

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQRADVDTCRMKGKHKDECHNF 12
|||||

Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEIYCSKKLTWKSQADVDTCRMKGHKDECHNF 120
Qy 121 IKVLLKKNDALFVCGTNAFNPSERNYKMDTLEPGDEFSGMARCPYDAKHANVALFADG 180
|||
Db 121 IKVLLKKNDALFVCGTNAFNPSERNYKMDTLEPGDEFSGMARCPYDAKHANVALFADG 180
Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
|||
Db 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
Qy 241 VEYNTMGKVVFPRAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
|||
Db 241 VEYNTMGKVVFPRAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
Qy 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
|||
Db 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
|||
Db 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
Qy 421 TKIADVTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD 480
|||
Db 421 TKIADVTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD 480
Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 540
|||
Db 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 540
Qy 541 ACHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESR 600
|||
Db 541 ACHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN----- 576
Qy 601 GGMLDWKHLLSPDSTDPLGAVSSHNNQDKKGVIRESYLKGHDLQLPVTLLAIAVILAFV 660
|||
Db 577 -----GVIRESYLKGHDLQLPVTLLAIAVILAFV 605
Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKEELTHSRRGSMSSVTKLSQLFGDTQSKDPKPE 720
|||
Db 606 MGAVFSGITVYCVCDHRRKDVAVVQRKEKEELTHSRRGSMSSVTKLSQLFGDTQSKDPKPE 665
Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLIDLPTPESTPTLQQKRKPSRGSREWERN 780
|||:
Db 666 AILTPLMHNGKLATPGNTAKMLIKADQHHLIDLPTPESTPTLQQKRKPSRGTREWERN 725
Qy 781 QNLINACTKDMPPMGSPIPTDPLRASPISHPSVVLPITQQGYQHEYVDQPKMSEVAQ 840
|||
Db 726 QNLINACTKDMPPMGSPIPTDPLRASPISHPSVVLPITQQGYQHEYVDQPKMSEVAQ 785
Qy 841 MALEDQAATLEYKTKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
|||
Db 786 MALEDQAATLEYKTKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 845
Qy 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQAT 932
|||
Db 846 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHLTT 877

RESULT 9
AAB95139
ID AAB95139 standard; protein; 699 AA.
XX
AC AAB95139;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:17154.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
XX
PS Claim 8; SEQ ID NO 17154; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX

SQ Sequence 699 AA;

Query Match 67.5%; Score 3677; DB 4; Length 699;
Best Local Similarity 100.0%; Pred. No. 1.2e-307;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 MLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF 391
Db 1 MLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF 60

Qy 392 IKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIIILKFL 451
Db 61 IKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIIILKFL 120

Qy 452 ARIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP 511
Db 121 ARIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP 180

Qy 512 LGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS 571
Db 181 LGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS 240

Qy 572 FVALNGHSSLLPSTTSDDSTAQEYESRGMLDWKHLLDSDPSTDPLGAVSSHNHQDKK 631
Db 241 FVALNGHSSLLPSTTSDDSTAQEYESRGMLDWKHLLDSDPSTDPLGAVSSHNHQDKK 300

Qy 632 GVIRESYLGHDLQKLPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKEL 691
Db 301 GVIRESYLGHDLQKLPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKEL 360

Qy 692 THSRRGSMSSVTKLSGLFGDTQS KDPKPEA ILTPLMHNGKLATPGNTAKMLIKA DQHHL 751
Db 361 THSRRGSMSSVTKLSGLFGDTQS KDPKPEA ILTPLMHNGKLATPGNTAKMLIKA DQHHL 420

Qy 752 LTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDPLRASP 811
Db 421 LTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDPLRASP 480

Qy 812 IPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPN HGVNL 871
Db 481 IPSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPN HGVNL 540

Qy 872 ENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA 931
Db 541 ENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA 600

Qy 932 TTLKRNNNTNSSSSHL SRNQSFGRGDNP PPAQ RVDSIQVHSSQPSGQAVTVSRQPSLNA 991
Db 601 TTLKRNNNTNSSSSHL SRNQSFGRGDNP PPAQ RVDSIQVHSSQPSGQAVTVSRQPSLNA 660

Qy 992 YNSLTRSGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT 1030
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 YNSLTRSGLKRTPSLKPDPVPPKPSFAPLSTSMKPNDACT 699

RESULT 10
AAB23043
ID AAB23043 standard; protein; 630 AA.
XX
AC AAB23043;
XX
DT 16-JAN-2001 (first entry)
XX
DE Human semaphorin protein-like splice variant, SECX pCR2.1-2864933.
XX
KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200053742-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US006280.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 08-MAR-2000; 2000US-0520781P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA;
XX
DR WPI; 2000-594318/56.
DR N-PSDB; AAA93630.
XX
PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.
XX
PS Claim 1; Fig 15; 15lpp; English.
XX
CC Sequences AAB23029-B23048 represent human SECX proteins. The SECX
CC proteins of the invention are either secreted or membrane-associated
CC proteins and act as regulator of cellular proliferation and
CC differentiation. SECX proteins or nucleotides are useful for diagnosing
CC the presence of, or predisposition to, a disease associated with altered

CC levels of SECX proteins and nucleotides. The SECX proteins are also
CC useful to screen compounds that modulate SECX activity or expression. The
CC interaction of a SECX protein with other cellular proteins may be useful
CC to modulate the activity of a partner protein, cellular proliferation,
CC cellular differentiation and cell survival. SECX nucleotides are useful
CC for the recombinant expression of SECX protein, and may be used detect
CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to
CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX
CC nucleic acid sequences are also useful for identifying a cell or tissue
CC type in a biological sample, and in forensic biology. SECX primers or
CC probes are useful for detecting the presence of SECX nucleotides and for
CC screening tissue cultures for contamination. Diseases that may be treated
CC or prevented using SECX proteins or nucleotides include cancer (e.g.,
CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
CC or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 630 AA;

Query Match 61.9%; Score 3373; DB 3; Length 630;
Best Local Similarity 99.8%; Pred. No. 1.8e-281;
Matches 628; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 17 GAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI 76
|:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GSGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI 60

Qy 77 YTVIDITSHTEEIYCSKKLTWKSQADVDCRMKGKHDECHNFIKVLLKKNDALFVCG 136
|||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 YTVIDITSHTEEIYCSKKLTWKSQADVDCRMKGKHDECHNFIKVLLKKNDALFVCG 120

Qy 137 TNAFNPSCKNYKMDTLEPFGDEFSGMARCPTYDAKHANVALFADGKLYSATVTDFLAIDAV 196
|||||||||||||||||||||||||||||||||||||||||||||
Db 121 TNAFNPSCKNYKMDTLEPFGDEFSGMARCPTYDAKHANVALFADGKLYSATVTDFLAIDAV 180

Qy 197 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFREIAVEYNTMGKVVFPRVAQ 256
|||||||||||||||||||||||||||||||||||||||||
Db 181 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFREIAVEYNTMGKVVFPRVAQ 240

Qy 257 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 316
|||||||||||||||||||||||||||||||||||||
Db 241 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 300

Qy 317 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSLE 376
|||||||||||||||||||||||||||||||||||||
Db 301 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSLE 360

Qy 377 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT 436
|||||||||||||||||||||||||||||||||
Db 361 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT 420

Qy 437 VVFLGSEKGIIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS 496
|||||||||||||||||||||||||||||||||
Db 421 VVFLGSEKGIIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS 480

Qy 497 SSLYVAFSTCVIKVPLGRKERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLTSEQD 556
|||
Db 481 SSLYVAFSTCVIKVPLGRKERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLTSEQD 540

Qy 557 IERGNTDGLGDCHNSFVALNGHSSSLPSTTSSTAQEGYESRGGMLDWKHLLDSPDST 616
|||
Db 541 IERGNTDGLGDCHNSFVALNGHSSSLPSTTSSTAQEGYESRGGMLDWKHLLDSPDST 600

Qy 617 DPLGAVSSHNHQDKKGVIRESYLNKHDQL 645
|||
Db 601 DPLGAVSSHNHQDKKGVIRESYLNKHDQL 629

RESULT 11

ADA23307

ID ADA23307 standard; protein; 630 AA.

XX

AC ADA23307;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
KW cardiovascular disease; oncology disease; immune disorder;
KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological.

XX

OS Homo sapiens.

XX

PN US2003054514-A1.

XX

PD 20-MAR-2003.

XX

PF 19-SEP-2001; 2001US-00957187.

XX

PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.

XX

PA (SHIM/) SHIMKETS R A.

PA (LARO/) LAROCHELLE W J.

XX

PI Shimkets RA, Larochelle WJ;

XX

DR WPI; 2003-540616/51.

DR N-PSDB; ADA23306.

XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 12; Fig 15; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence represents a
CC SECX polypeptide of the invention.

XX
SQ Sequence 630 AA;

Query Match 61.9%; Score 3373; DB 6; Length 630;
Best Local Similarity 99.8%; Pred. No. 1.8e-281;
Matches 628; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 17 GAGFPEDSEPISISHGNYTKQYPVFGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI 76
Db 1 GSGFPEDSEPISISHGNYTKQYPVFGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI 60

Qy 77 YTVIDITSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHDECHNFIKVLLKKNDALFVCG 136
Db 61 YTVIDITSHTEEIYCSKKLTWKSQRQADVDTCRMKGKHDECHNFIKVLLKKNDALFVCG 120

Qy 137 TNAFN PSCR NYKMDTLE PFGDEFSGM ARCPY DAKHAN VALF ADGKL YSAT VTD FLA IDAV 196
Db 121 TNAFN PSCR NYKMDTLE PFGDEFSGM ARCPY DAKHAN VALF ADGKL YSAT VTD FLA IDAV 180

Qy 197 IYRSLGE SPTLRTV KHDSK WLKE PYFV QAVD YGDY IYFFF REIA VEY NTMG KVVF PRVAQ 256
Db 181 IYRSLGE SPTLRTV KHDSK WLKE PYFV QAVD YGDY IYFFF REIA VEY NTMG KVVF PRVAQ 240

Qy 257 VCKNDMGG SQRV LEKQ WTSFL KARLN C SVPGD SHFY FNIL QAVT DVIR IN GRDV VLATFS 316
Db 241 VCKNDMGG SQRV LEKQ WTSFL KARLN C SVPGD SHFY FNIL QAVT DVIR IN GRDV VLATFS 300

Qy 317 TPYNSIPGS AVCAYDML DIASVFTGR FKEQ KSPD STWT PVP DER VP KPR PGCC AGSSS LE 376
Db 301 TPYNSIPGS AVCAYDML DIASVFTGR FKEQ KSPD STWT PVP DER VP KPR PGCC AGSSS LE 360

Qy 377 RYATSNEFPDD TLNF IKTHPL MDEAVPSI FNRPWFL RTMVR YRLTKIAVDTAAGPYQNHT 436
Db 361 RYATSNEFPDD TLNF IKTHPL MDEAVPSI FNRPWFL RTMVR YRLTKIAVDTAAGPYQNHT 420

Qy 437 VVFLGSEKG IILKFLAR IGN SGF LND SLF LEEM SVN SEKCSY DGVED KRIM GMQL DRAS 496
Db 421 VVFLGSEKG IILKFLAR IGN SGF LND SLF LEEM SVN SEKCSY DGVED KRIM GMQL DRAS 480

Qy 497 SSLYVAFSTCVIKVPLGRGERHGCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTSEQD 556
|||
Db 481 SSLYVAFSTCVIKVPLGRGERHGCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTSEQD 540

Qy 557 IERGNTDGLGDCHNSFVALNGHSSLLPSTTSYSTAQEGYESRGGMWDWKHLLDSDST 616
|||
Db 541 IERGNTDGLGDCHNSFVALNGHSSLLPSTTSYSTAQEGYESRGGMWDWKHLLDSDST 600

Qy 617 DPLGAVSSHQDKKGVIRESYLYGHDL 645
|||
Db 601 DPLGAVSSHQDKKGVIRESYLYGHDL 629

RESULT 12

ADA23360

ID ADA23360 standard; protein; 626 AA.

XX

AC ADA23360;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human SECX polypeptide, SEC3 #2.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1; SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12; SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer; cardiovascular disease; oncology disease; immune disorder; autoimmune disease; transplant rejection; allergy; AIDS; infections; inflammatory disorder; arthritis; haematopoietic disorder; skin disorder; atherosclerosis; restenosis; neurological disease; Alzheimer's disease; trauma; wounds; spinal cord injury; skeletal disorder; cytostatic; antiinflammatory; immunosuppressive; anti-HIV; antiarthritic; antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary; antiallergic; cardiant; dermatological.

XX

OS Homo sapiens.

XX

PN US2003054514-A1.

XX

PD 20-MAR-2003.

XX

PF 19-SEP-2001; 2001US-00957187.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 04-JAN-2000; 2000US-0174485P.

PR 08-MAR-2000; 2000US-00520781.

PR 19-SEP-2000; 2000US-0233798P.

PR 20-SEP-2000; 2000US-0234082P.

XX

PA (SHIM//) SHIMKETS R A.

PA (LARO//) LAROCHELLE W J.

XX

PI Shimkets RA, Larochele WJ;

XX

DR WPI; 2003-540616/51.

DR N-PSDB; ADA23359.

XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 12; Page 7; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence represents a
CC SECX polypeptide of the invention.
XX
SQ Sequence 626 AA;

Query Match 61.7%; Score 3362; DB 6; Length 626;
Best Local Similarity 100.0%; Pred. No. 1.6e-280;
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHIYT 78
Db 1 GFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHIYT 60

Qy 79 VDIDTSHTEEIYCSKKLTWKS RQADVDTCRMKGKH DECHNFIKVLLKKNDDALFVCGTN 138
Db 61 VDIDTSHTEEIYCSKKLTWKS RQADVDTCRMKGKH DECHNFIKVLLKKNDDALFVCGTN 120

Qy 139 AFNPSCRNYKMDTLEPFGDEFSGMARC PYDAKHANVALFADGKLYSATVTDFLAIDAVIY 198
Db 121 AFNPSCRNYKMDTLEPFGDEFSGMARC PYDAKHANVALFADGKLYSATVTDFLAIDAVIY 180

Qy 199 RSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVEYNTMGKVV FPRVAQVC 258
Db 181 RSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVEYNTMGKVV FPRVAQVC 240

Qy 259 KNDMGGSQRVLEKQWTSFLKARLNCSV PGDSHFYFNILQAVTDVIRINGRDVVLATFSTP 318
Db 241 KNDMGGSQRVLEKQWTSFLKARLNCSV PGDSHFYFNILQAVTDVIRINGRDVVLATFSTP 300

Qy 319 YNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPV PDERVPKPRPGCCAGSSSLERY 378
Db 301 YNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPV PDERVPKPRPGCCAGSSSLERY 360

Qy 379 ATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR YRLTKIAVDTAAGPYQNHTVV 438
Db 361 ATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR YRLTKIAVDTAAGPYQNHTVV 420

Qy 439 FLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSS 498
Db 421 FLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSS 480

Qy 499 LYVAFSTCVIKVPLGRCERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLTSEQDIE 558
|||
Db 481 LYVAFSTCVIKVPLGRCERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLTSEQDIE 540

Qy 559 RGNTDGLGDCHNSFVALNGHSSSLPSTTSSTAQEGYESRGGMLDWKHLLDSPDSTD 618
|||
Db 541 RGNTDGLGDCHNSFVALNGHSSSLPSTTSSTAQEGYESRGGMLDWKHLLDSPDSTD 600

Qy 619 LGAVSSHNHQDKKGVIRESYLGHDQ 644
|||
Db 601 LGAVSSHNHQDKKGVIRESYLGHDQ 626

RESULT 13

AAB95317

ID AAB95317 standard; protein; 574 AA.

XX

AC AAB95317;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:17568.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX

PS Claim 8; SEQ ID NO 17568; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the

CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX

SQ Sequence 574 AA;

Query Match 54.7%; Score 2980.5; DB 4; Length 574;
Best Local Similarity 90.7%; Pred. No. 1.2e-247;
Matches 574; Conservative 0; Mismatches 0; Indels 59; Gaps 1;

Qy 398 MDEAVPSIFNRPWFLRTMVRYLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNS 457
Db 1 MDEAVPSIFNRPWFLRTMVR----- 20

Qy 458 GFLNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcer 517
Db 21 -----CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcer 61

Qy 518 HGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG 577
Db 62 HGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNG 121

Qy 578 HSSSLPSTTSDSTAQEYESRGMLDWKHLLSPDSTDPLGAVSSHNHQDKKGVIRES 637
Db 122 HSSSLPSTTSDSTAQEYESRGMLDWKHLLSPDSTDPLGAVSSHNHQDKKGVIRES 181

Qy 638 YLKGDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRG 697
Db 182 YLKGDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRG 241

Qy 698 SMSSVTKLSGLFGDTQS KDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLTLPT 757
Db 242 SMSSVTKLSGLFGDTQS KDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLTLPT 301

Qy 758 PESTPTLQQKRKP SRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASP SHIPS VVV 817
Db 302 PESTPTLQQKRKP SRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASP SHIPS VVV 361

Qy 818 LPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLS SKSPN HGVNLVENLDSL 877
Db 362 LPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLS SKSPN HGVNLVENLDSL 421

Qy 878 PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRN 937
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 422 PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRN 481

Qy 938 NTNSSNSSHLSRNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR 997
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 482 NTNSSNSSHLSRNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR 541

Qy 998 SGLKRTPSLKPVDVPPKPSFAPLSTSMKPNDACT 1030
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 542 SGLKRTPSLKPVDVPPKPSFAPLSTSMKPNDACT 574

RESULT 14

AAB94104

ID AAB94104 standard; protein; 562 AA.

XX

AC AAB94104;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:14328.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX

PS Claim 8; SEQ ID NO 14328; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the

CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX

SQ Sequence 562 AA;

Query Match 54.2%; Score 2952; DB 4; Length 562;
Best Local Similarity 100.0%; Pred. No. 3.2e-245;
Matches 562; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 469 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCRERHGKCKKTCIAS 528
Db 1 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCRERHGKCKKTCIAS 60

Qy 529 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTT 588
Db 61 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTT 120

Qy 589 SDSTAQEYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLGHDQLVPV 648
Db 121 SDSTAQEYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLGHDQLVPV 180

Qy 649 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGL 708
Db 181 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGL 240

Qy 709 FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLTLALPTPESTPTLQQKR 768
Db 241 FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLTLALPTPESTPTLQQKR 300

Qy 769 KPSRGSREWERNQNLINACTKDMPPMGSIVIPTDLPLRASPISHIPSVVLPITQQGYQHE 828
Db 301 KPSRGSREWERNQNLINACTKDMPPMGSIVIPTDLPLRASPISHIPSVVLPITQQGYQHE 360

Qy 829 YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHNVLVENLDSLPPKVPQREASL 888
Db 361 YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHNVLVENLDSLPPKVPQREASL 420

Qy 889 GPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSSLHS 948
Db 421 GPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSSLHS 480

Qy 949 RNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 1008
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 RNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 540

Qy 1009 DVPPKPSFAPLSTSMKPNDACT 1030
||| ||| ||| ||| ||| |||
Db 541 DVPPKPSFAPLSTSMKPNDACT 562

RESULT 15

AAM93444

ID AAM93444 standard; protein; 562 AA.

XX

AC AAM93444;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide, SEQ ID NO: 3088.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-00114089.

XX

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

DR WPI; 2001-524255/58.

DR N-PSDB; AAK94365.

XX

PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.

XX

PS Claim 8; SEQ ID NO 3088; 1380pp + Sequence Listing; English.

XX

CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO

XX

SQ Sequence 562 AA;

Query Match 54.1%; Score 2947; DB 4; Length 562;
Best Local Similarity 99.8%; Pred. No. 8.7e-245;
Matches 561; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 469 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGCKKTCIAS 528
Db 1 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGCKKTCIAS 60

Qy 529 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTT 588
Db 61 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTT 120

Qy 589 SDSTAQEYESRGGMWDWKHLLSPDSTDPLGAVSSHNDKKGVIRESYLGHDQLVPV 648
Db 121 SDSTAQEYESRGGMWDWKHLLSPDSTDPLGAVSSHNDKKGVIRESYLGHDQLVPV 180

Qy 649 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGL 708
Db 181 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGL 240

Qy 709 FGDTQS KDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKR 768
Db 241 FGDTQS KDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKR 300

Qy 769 KPSRGSREWERNQNLI NACTKDMP PMGSPV I PTDLPLRASP SHIPS VVLP ITQQGYQHE 828
Db 301 KPSRGSREWERNQNLI NACTKDMP PMGSPV I PTDLPLRASP SHIPS VVLP ITQQGYQHE 360

Qy 829 YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPN HGVNLVENLDSLPPKVPQREASL 888
Db 361 YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPN HGVNLVENLDSLPPKVPQREASL 420

Qy 889 GPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLS 948
Db 421 GPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLS 480

Qy 949 RNQSFGRGDNP PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNLSRGLKRTPSLKP 1008
Db 481 RNQSFGRGDSP PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNLSRGLKRTPSLKP 540

Qy 1009 DVPPKPSFAPLSTS MKPND ACT 1030
Db 541 DVPPKPSFAPLSTS MKPND ACT 562

Search completed: March 24, 2004, 13:14:21
Job time : 104.009 secs

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OM protein - protein search, using sw model

Run on: March 24, 2004, 13:12:28 ; Search time 32.7132 Seconds
(without alignments)
1625.481 Million cell updates/sec

Title: US-09-856-681A-2

Perfect score: 5450

Sequence: 1 MRSEALLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2361.5	43.3	1086	4	US-09-653-274-4	Sequence 4, Appli
2	2354	43.2	1070	4	US-09-653-274-8	Sequence 8, Appli
3	2013.5	36.9	888	4	US-09-077-940A-4	Sequence 4, Appli
4	1997	36.6	887	4	US-09-077-940A-2	Sequence 2, Appli
5	1923	35.3	641	4	US-09-653-274-13	Sequence 13, Appli
6	1519.5	27.9	930	4	US-09-254-594-6	Sequence 6, Appli
7	1428.5	26.2	929	4	US-09-254-594-3	Sequence 3, Appli
8	1377.5	25.3	536	4	US-09-653-274-10	Sequence 10, Appli
9	969.5	17.8	730	1	US-08-121-713D-58	Sequence 58, Appli
10	969.5	17.8	730	1	US-08-835-268-58	Sequence 58, Appli
11	969.5	17.8	730	2	US-09-060-692-58	Sequence 58, Appli

12	969.5	17.8	730	3	US-08-833-391-58	Sequence 58, Appl
13	969.5	17.8	730	4	US-09-060-610-58	Sequence 58, Appl
14	969.5	17.8	730	5	PCT-US94-10151A-58	Sequence 58, Appl
15	880	16.1	650	1	US-08-121-713D-60	Sequence 60, Appl
16	880	16.1	650	1	US-08-835-268-60	Sequence 60, Appl
17	880	16.1	650	2	US-09-060-692-60	Sequence 60, Appl
18	880	16.1	650	3	US-08-833-391-60	Sequence 60, Appl
19	880	16.1	650	4	US-09-060-610-60	Sequence 60, Appl
20	880	16.1	650	5	PCT-US94-10151A-60	Sequence 60, Appl
21	852.5	15.6	655	4	US-08-556-422A-3	Sequence 3, Appli
22	852.5	15.6	771	1	US-08-121-713D-54	Sequence 54, Appl
23	852.5	15.6	771	1	US-08-835-268-54	Sequence 54, Appl
24	852.5	15.6	771	2	US-09-060-692-54	Sequence 54, Appl
25	852.5	15.6	771	3	US-08-833-391-54	Sequence 54, Appl
26	852.5	15.6	771	4	US-09-060-610-54	Sequence 54, Appl
27	852.5	15.6	771	5	PCT-US94-10151A-54	Sequence 54, Appl
28	845	15.5	712	1	US-08-121-713D-64	Sequence 64, Appl
29	845	15.5	712	1	US-08-835-268-64	Sequence 64, Appl
30	845	15.5	712	2	US-09-060-692-64	Sequence 64, Appl
31	845	15.5	712	3	US-08-833-391-64	Sequence 64, Appl
32	845	15.5	712	4	US-09-060-610-64	Sequence 64, Appl
33	845	15.5	712	5	PCT-US94-10151A-64	Sequence 64, Appl
34	779.5	14.3	724	1	US-08-121-713D-62	Sequence 62, Appl
35	779.5	14.3	724	1	US-08-835-268-62	Sequence 62, Appl
36	779.5	14.3	724	2	US-09-060-692-62	Sequence 62, Appl
37	779.5	14.3	724	3	US-08-833-391-62	Sequence 62, Appl
38	779.5	14.3	724	4	US-09-060-610-62	Sequence 62, Appl
39	779.5	14.3	724	5	PCT-US94-10151A-62	Sequence 62, Appl
40	748	13.7	775	4	US-09-308-179B-1	Sequence 1, Appli
41	736.5	13.5	862	4	US-08-556-422A-2	Sequence 2, Appli
42	654.5	12.0	607	4	US-08-556-422A-4	Sequence 4, Appli
43	586	10.8	477	1	US-08-136-922-2	Sequence 2, Appli
44	539	9.9	425	4	US-08-556-422A-7	Sequence 7, Appli
45	462	8.5	295	4	US-08-556-422A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-653-274-4

```
; Sequence 4, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides
; FILE REFERENCE: HYS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
```

; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-653-274-4

Query Match 43.3%; Score 2361.5; DB 4; Length 1086;
Best Local Similarity 45.5%; Pred. No. 2.2e-215;
Matches 512; Conservative 159; Mismatches 308; Indels 147; Gaps 30;

Qy 1 MRSEALLLYFTLL---HFAGAGFPEDSEPIISIHGNYTKQYPVFVGHKGPRNTTQRHRLD 57
Db 1 MRVFLLCAYILLMVSQRLAVSFPEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLD 58

Qy 58 IQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRADVDTCRMKGHKDEC 117
Db 59 FQLMLKIRDTLIAGRQVYTVNLNEMPKTEVIPNKKLTWRSRQQDRENCAMKGHKDEC 118

Qy 118 HNFIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALF 177
Db 119 HNFIKVFPVRNDEMVFVCGTNAFNPMCRYRLSTLEYDGEISGLARCPFDARQTNVALF 178

Qy 178 ADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLEPYFVQAVDYGDYIYFFR 237
Db 179 ADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIETYGNVYFFR 238

Qy 238 EIAVEYNTMGKVVFPRAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQ 297
Db 239 EIAVEHNNLGKAVYSRVARICKNDMGGSSQRVLEKHWTSFLKARLNCSVPGDPFFYFDVLQ 298

Qy 298 AVTDVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
Db 299 SITDIIQINGIPTVVGVFTQLNSIPGSACAFSMDDIEKVFKGRFKEQKTPDSDVWTAVP 358

Qy 358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
Db 359 EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSFIKSHPLMDSAVPPIADEPWFTKTRVR 418

Qy 418 YRLTKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGF-LNDSLFLLEMSVYNSEK 476
Db 419 YRLTAISVDHSAGPYQNYTVIFVGSEAGMVLKVLAK--TSPFSLNDSVLEEIEAYNHAK 476

Qy 477 CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWI 536
Db 477 CSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERYGSCKKSCIASRDPYCGWL 536

Qy 537 KEGGACSHLSPNSRLT-----FEQDIERGNTDGLGDCHNSFVALNGHSSL 582
Db 537 SQ-GSCGRVTPGMLLTEDFFAFHNHSAEGYEQDTEFGNTAHLGDCH-----EI 584

Qy 583 LPSTTTSDSTAQEYESRGG-----MLD-WKHLL----- 610
Db 585 LPTSTTPD-----YKIFGGPTSDMEVSSSSVTTMASIPEITPKVIDTWRPKLTSSRKFV 638

RESULT 2

US-09-653-274-8

; Sequence 8, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

APPLICANT: Boyle, Bryan J

APPLICANT: Yeung, George

APPLICANT: Arterburn, Ma

APPLICANT: Mize, Nancy K

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Drmanac, Rado

TITLE OF INVENTION: Meth-

: TITLE OF INVENTION: Polypeptides and Polynucleotides

FILE REFERENCE: HYS-23

: CURRENT APPLICATION NUM

CURRENT FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: 09/49

PRIOR APPLICATION NUMBER: 09/491,401

NUMBER OF SEQ ID NOS: 13

NUMBER OF SEQ ID NOS.: 15
SOFTWARE: PatentIn Ver. 3

; SOFTWARE. Patent in Ver. 2.1
; SEQ ID NO: 8

, SEQ ID NO 8

; LENGTH: 1070
; TYPE: DBT

; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-653-274-8

Query Match 43.2%; Score 2354; DB 4; Length 1070;
Best Local Similarity 45.8%; Pred. No. 1.1e-214;
Matches 506; Conservative 159; Mismatches 295; Indels 144; Gaps 29;

Qy 20 FPEDSEPISHGNYTKQYPVFGHKGPRNTTQRHRLDIQMIMIMNGTLYIAARDHIYTV 79
Db 7 FPEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLDFQLMLKIRDTLYIAGRQVYTV 64

Qy 80 DIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHDECHNFIKVLLKKNDALFVCGTNA 139
Db 65 NLNEMPKTEVIPNKKLTWRSRQQDRENCAKGKHDECHNFIKVFPVRNDEMVFVCGTNA 124

Qy 140 FNPSCKNYKMDTLEPFGDEFSGMARCYDAKHANVALFADGKLYSATVTDFLAIDAVIYR 199
Db 125 FNPMCRYRLSTLEYDGEIISGLARCPFDARQTNVALFADGKLYSATVADFLASDAVIYR 184

Qy 200 SLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRAQVCK 259
Db 185 SMGDGSALRTIKYDSKWIKEPHFLHAEYGNVYFFFREIAVEHNNLGKAVYSRVARICK 244

Qy 260 NDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFSTPY 319
Db 245 NDMGGSQRVLEKHWTSDLKARLNCSVPGDPFFYFDVLQSITDIIQINGIPTVVGFTTQL 304

Qy 320 NSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYA 379
Db 305 NSIPGSACVAFSMDIEKVFGRFKEQKTPDSVWTAVPEDKVPKPRPGCCAHKGLAEAYK 364

Qy 380 TSNEFPDDTLNFIFKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVF 439
Db 365 TSIDFPDETLSFIKSHPLMDSAVPPPIADEPWFTKTRVRYRLTAISVDHSAGPYQNYTVIF 424

Qy 440 LGSEKGIILKFLARIGNSGF-LNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSS 498
Db 425 VGSEAGMVLKVLAK--TSPFSLNDSVLEEIEAYNHAKCSAENEEDKKVISLQLDKDHHA 482

Qy 499 LYVAFSTCVIKVPLGRCRERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLT----- 552
Db 483 LYVAFSSCIIRIPLSRCERYGSCKSCIASRDPYCGWLSQ-GSCGRVTGMLLTEDFFA 541

Qy 553 -----FEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQEYERSRGG-- 602
Db 542 FHNHSAEGYEQDTEFGNTAHLGDCH-----EILPTSTTPD-----YKIFGGPT 584

Qy 603 -----MLD-WKHLL-----DSP---DSTDPLGAVSSHNN 627
Db 585 SDMEVSSSSVTTMASIPEITPKVIDTWRPKLTSSRKFVVQDDPNTSDFTDPLSGI----- 639

Qy 628 QDKKGVIRESYLKGHDQLVPVTLLAIAVILAFAVMGAVFSGITVYCVCD-HRRKDVAVVQR 686
Db 640 --PKGVRWEVQSGESNQMVHMNVLITCVFAAFVLGAFIAGVAVYCYRDMFVRKNRKI--H 695

Qy 687 KEKELTHSRRGSMSSVTLSGLFG---DTQSKDPKPEAILTPLMHNGKLATPGNTAKML 742
|: | | | | ||::|| : | |: | | : | |: | |:

Db 696 KDAESAQSCTDSSGSFAKLNGLFDSPVKEYQQNIDSPLYSNLTSRKELPPNGDTKSMV 755
 Qy 743 IKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERNQNLLINACTKDMPPMGSPVIPTD 802
 : : | ||||||| | | : | : : | | : | : |
 Db 756 MDHRGQPPELAALPTPESTPVLHQTLQAMKSHSEKAHGH--GASRKETPQFFPSSPPPH 813
 Qy 803 LPLRASPSPHSVVVLPIQQGYQHEY-----VDQP---KMSEVAQMALED 845
 || | |||| : || | : : | | : | : | : |
 Db 814 SPL--SHGHIPSAIVLPNATHDYNTSFNSNAHKAEKKLQNIIDHPLTKSSSKRDHRRSVD 871
 Qy 846 QAATLEYKTIKEHLSSKSPN-----HGVNLVENLDSL---PPKVPQREASLGPP 891
 || : : || : | : | : : | : | : | : | : |
 Db 872 SRNTL--NDLLKHLNDPNSNPKAIMGDIQMAHQNLMLDPGMSMSEVPPKVPNREASLYSP 929
 Qy 892 GASLSQTGLSKRLEMHHSSY---GVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLS 948
 ::| : : ||:: : : : | | || | | : : | || | ||
 Db 930 PSTLPRNSPTKRVDVPTPGVPMTSLERQRGYHKNSSQR-HSISAMPK-NLNSPNGVLLS 987
 Qy 949 RNQSFGRGD-NPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT----RSGLK 1001
 | | | | | | : || | | : | : | | : | | : | : ||
 Db 988 RQPSMNRRGGYMPTPTGAKVDYIQ-----GTPVSVHLQPSLSRQSSYTSNGTLPRTGLK 1040
 Qy 1002 RTPSLKPDVPPKPSFAPLSTMKP 1025
 ||||| | | | | | | | : | : |
 Db 1041 RTPSLKPDVPPKPSFVQTPSVRP 1064

RESULT 3

US-09-077-940A-4

; Sequence 4, Application US/09077940A
 ; Patent No. 6576441
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMURA, Toru et al.
 ; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
 ; FILE REFERENCE: 0020-4426P
 ; CURRENT APPLICATION NUMBER: US/09/077,940A
 ; CURRENT FILING DATE: 1998-06-05
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 888
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-077-940A-4

Query Match 36.9%; Score 2013.5; DB 4; Length 888;
 Best Local Similarity 45.3%; Pred. No. 2.3e-182;
 Matches 424; Conservative 129; Mismatches 241; Indels 141; Gaps 20;

Qy 5 ALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQR--HRLDIQMIM 62
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 Db 12 ALLLLLLLGGAHGLFPEDPPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGADDLNIQRVL 71
 Qy 63 IMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVTCRMKGKHDECHNFIK 122
 : | | : | | | : | : | : | : | : | : | : | : | : | : |
 Db 72 RVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGERNFVK 131

Qy	123	VLLKKNDALFVCGTNAFPNSCRNYKMDTLEPGDFSGMARCPCYDAKHANVALFADGKL	182
:::: : : :			
Db	132	VLLLRDESTLFVCGSNAFPVCANYSIDTLQPVGDNISGMARCPYDPKHKANVALFSDGML	191
::			
Qy	183	YSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVE	242
:			
Db	192	FTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREIAAME	251
:			
Qy	243	YNTMGKVVFPRTVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDHFYFNILQAVTDV	302
: :			
Db	252	FNYLEKVVSVRVARVCKNDVGGSPRVLQWTSFLKARLNCSVPGDHFYFNVLQAVTGV	311
:			
Qy	303	IRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWT PVPDERVP	362
: :			
Db	312	VSLGGRPVVLAVFSTPSNSIPGSACFDLTQVAVFEGRFREQQKSPESIWT PVPEDQVP	371
:			
Qy	363	KPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTK	422
:			
Db	372	RPRPGCCAAPGM--QYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWIRTL TLMRHQLTR	429
:			
Qy	423	IAVDTAAGPYQNHTVVFLGSEKGIILKFLAR--IGNSGFLNDSLFLLEEMSVYNSEKCSYD	480
:			
Db	430	VAVDVGAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTGLSVFLEEFETYRPDRCGRP	489
: :			
Qy	481	GVED--KRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKTCIASRDPYCGWIKE	538
: : :			
Db	490	GGGETGQRLLSLELDAASGGLLAAPRCVVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPD	549
: :			
Qy	539	GGACSHLSPNSRLTFFEODIERGNTDGLGDCHNSFVALNGHSSSLPSTTS DSTAQE GYE	598
:			
Db	550	-GSCIFLSPGTRAAFEQDVSGASTSGLGDC-----	578
: :			
Qy	599	SRGGMLDWKHL LDSPDSTDPLGAVSSH NHQDKKGVIRESY LKGHDQLVPVTLLAI A VILA	658
:			
Db	579	-----TGLLRASLSED RAGLVSVNLLV TSSVAA	606
: :			
Qy	659	FVMGAVFSGITV-YCVCDHRRKDVAVVQRKEKE--LTHSRRGSMSSVT KLSGLFGDT QSK	715
:			
Db	607	FVVGAVVSGFSGFWVGLRER RELA--RRKDKEA I LAHGAGEA VLSV SRL---GERRAQ	660
:			
Qy	716	DP-----KPEAILTPLMHNGKLATPGNTAK-MLIKADQHHDLTALPTPEST	761
Db	661	GPGGRGGGGGGGGAGVPPE ALLAPLMQNG-----WAKATLLQGGPHDLSG LLPTPEQT	713
Qy	762	PTIQQKRP-----SRGSREWERNQNLINACTKDMPPM GSPVIPTDLP---LRASPSH	811
Db	714	P-LPQKRLPTPHPHALGPRAWDH-----GHPLLPASASSLLL LAPAR	757
Qy	812	I PSVVVLPI TQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPN HGVNL V	871
Db	758	APEQPPAPGEPTPDGRLYAAPGRASHGDFPLTPHAS PDRRRV V-----SAPT GPLDPA	811
Qy	872	ENLDSLP-PKVPQREASL-----GPPGASLSQT	898
Db	812	SAADGLPPRWPSSPPGTGS LRRPLGPHAPPAATL RRT	846

RESULT 5

US-09-653-274-13

; Sequence 13, Application US/09653274

; Patent No. 6635742

GENERAL INFORMATION:

APPLICANT: Boyle, Bryan J

APPLICANT: Yeung, George Y

APPLICANT: Arterburn, Matt

APPLICANT: Mize, Nancy K

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

: APPLICANT: Drmanac, Radoje T

TITLE OF INVENTION: Methods and Materials Relating

TITLE OF INVENTION: Po

FILE REFERENCE: HYS-23

CURRENT APPLICATION NUMBER: US/0

CURRENT FILING DATE: 2000-08-31

PBTOR APPLICATION NUMBER: Q

PRIOR APPLICATION NUMBER:

PRIVILEGED COPY. 2003-01
NUMBER OF SEQ ID NOS: 13

**NUMBER OF S.
SOFTWARE:**

100-13074-1
; SEO ID NO. 13

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-653-274-13

Query Match 35.3%; Score 1923; DB 4; Length 641;
Best Local Similarity 55.3%; Pred. No. 5.5e-174;
Matches 362; Conservative 101; Mismatches 118; Indels 74; Gaps 12;

Qy 20 FPEDSEPISHGNYTKQYPVFGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHIYTV 79
Db 7 FPEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLDFQLMLKIRDTLIAGRQVYTV 64

Qy 80 DIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHDECHNFIKVLLKNDDALFVCGTNA 139
Db 65 NLNEMPKTEVIPNKKLTWRSRQQDRENCAKGKHDECHNFIKVFVPRNDEMVFVCGTNA 124

Qy 140 FNPSCKNYKMDTLEPGDEFSGMARCYDAKHANVALFADGKLYSATVTDLAIADAVIYR 199
Db 125 FNPMCRYYLSTLEYDGEELISGLARCPFDARQTNVALFADGKLYSATVADFLASDAVIYR 184

Qy 200 SLGESPTLRTVKHDSKWLKEPYFVQAVDYGYIYFFFREIAVEYNTMGKVVFPRAQVCK 259
Db 185 SMGDGSALRTIKYDSKWIKEPHFLHAIETYGNVYFFFREIAVEHNNLGKAVYSRVARIICK 244

Qy 260 NDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFSTPY 319
Db 245 NDMGGSQRVLEKHWTSFLKARLNCSVPGDPFFYFDVLQSITDIIQINGIPTVVGFTTQL 304

Qy 320 NSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYA 379
Db 305 NSIPGSACVAFSMDIEKVFGRFKEQKTPDSWTAVPEDKVPKPRPGCCAHKGLAEAYK 364

Qy 380 TSNEFPDDTLNFIFKTHPLMDEAVPSIFNRPWFRLTMVRYRLTKIAVDTAAGPYQNHTVVF 439
Db 365 TSIDFPDETLSFIKSHPLMDSAVPPIADEPWFTKTRVRYRLTAISVDHSAGPYQNYTVIF 424

Qy 440 LGSEKGIILKFLARIGNSGF-LNDSLFLLEMSVYNSEKCSYDGVEDKRIMGMQLDRASSS 498
Db 425 VGSEAGMVLKVLAK--TSPFSLNDSVLEEIEAYNHAKCSAENEEDKKVISLQLDKDHHA 482

Qy 499 LYVAFSTCVIKVPLGRCRERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLT----- 552
Db 483 LYVAFSSCIIRIPLSRCERYGSCKSCIASRDPYCGWLSQ-GSCGRVTGMLLTEDFFA 541

Qy 553 -----FEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQEYESRGG-- 602
Db 542 FHNHSAEGYEQDTEFGNTAHLGDCH-----EILPTSTTPD-----YKIFGGPT 584

Qy 603 -----MLD-WKHLL-----DSP---DSTDPLGAV 622
Db 585 SDMEVSSSSVTTMASIPEITPKVIDTWRPKLTSSRKFVVQDDPNTSDFTDPLSGI 639

RESULT 6
US-09-254-594-6
; Sequence 6, Application US/09254594
; Patent No. 6566094

; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()...()
; OTHER INFORMATION: Tissue Type: Child Brain
; NAME/KEY: misc_feature
; LOCATION: ()...()
; OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-6

Query Match 27.9%; Score 1519.5; DB 4; Length 930;
Best Local Similarity 35.9%; Pred. No. 3.2e-135;
Matches 381; Conservative 135; Mismatches 356; Indels 189; Gaps 32;

Qy 6 LLLYFTLLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMN 65
||| :|| | | ||:| |:|| | | | | : :|| | :||| : :|||
Db 13 LLLLLSLPH-TQAAFPQDPLPLLISDLQGTSPLSWFRGLEDDAVAAEL-GLDFQRFILTIN 70

Qy 66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSQADVDTCRMKGKHDECHNFIKVL 124
|| :|||||:::|:| :| :| |||:|:| :||| | ::|| | |||:|:|:|||
Db 71 RTLLVAARDHVFSFDLQAEEGEGEGLVPNKYLTWRSQ--DVENCARVGKLTDECYNYIRVL 128

Qy 125 LKKNDDALFVCGTNAFNPSERNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYS 184
: | | |||:|:| ||:| :|:| | |||:|| | :|||:||:| |||
Db 129 VPWDSQTLLACGTNSFSPVCRSYGITSLQQEGEELSGQARCPFDATQSNVAIFAEGLYS 188

Qy 185 ATVTDFAIDAVIYRSLGESPTLRTVKHD SKWLKEPYFVQAVDYGDYIYFFFREIAVEYN 244
|| | | | |||:|||| | ||:| :| |||:|:|:|:|:|:|:|:|:|||
Db 189 ATAADFQASDAVYRSLGPQPPLRSAKYDSKWLREPHFVQALEHGDHVYFFFREVSVEDA 248

Qy 245 TMGVVFPRVAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIR 304
:||| | | |||:||| | ||| | |::| |||:||| | |||:|||:| :|
Db 249 RLGKVQFSRVARVCKRDGGSPRALDRHWTSLKLRLNCVPGDSTFYFDVLQALTGPVN 308

Qy 305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKP 364
::| | : | :| | |||:|||:| :| | |:|:|:| | | | :| ||| |
Db 309 LHGRSALFGVFTTQTNSIPGSAVCAFYLDEIERGFEGKFKEQRSLDGAWT PVS EDRVPSP 368

Qy 365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA 424
||| | | | :| :| | | | | |||:| | | | :| :| | | | | | | :|
Db 369 RPGSCAGVGGAA LFSSSRDLPDDVLTIFIKAHPLLDPAVPPVTHQP-LLT LTSR ALLTQVA 427

Qy 425 VDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFL EEMSVYNSEKCSYDGVED 484
|| | ||:| | ||:|||| | :| | | | | | :| :| | :| :| :|
Db 428 VDG MAGPHSNITVMFLGSNDGTVLKVLT PGGRS GG-PEPIL LEEIDAYS PARCS GKR TAQ 486

QY 485 --KRIMGMQLDRASSSLYVAFSTCVIKVPLGRGERHGCKKTCIASRDPYCGWIKEGGAC 542
 :||:||::|| |:|||| ||::|| || || || |::||:|||:|| | |
 Db 487 TARRIIGLELDTEGHRLFVAFSGCIVYLPLSRCARHGACQRSCLASQDPYCGWHSSRG-C 545
 Qy 543 SHLSPNSRLTFFEQDIERGNTDGL--GDCHNSFVALNGHSSSLPSTTSSTAQEGYESR 600
 : : : | || : || | : : | | : | : | |
 Db 546 VDIRGSGGTDVDQ---AGNQESMEHGDCQDG-----ATGSQSGPGDSAY--- 586
 Qy 601 GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLYKGHDQLVPVTLLAIAVILAFV 660
 || | : : ||: || : | || |
 Db 587 -----GVRRDLPPASASRSVPPIPLLASVAAAFA 615
 Qy 661 MGAVFSGITVYCVCDHRRKDVAVQRKEKELTHSRRG-----SMSVTKLGL 708
 :|| ||: || | || | | || | | | | : | : || |
 Db 616 LGASVSGLLVSCAC--RR-----AHRRRGKDIETPGLPRPLSLRSLARLHG- 659
 Qy 709 FGDTQS KDPKP--EAI LTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQ 766
 | : | : || :: | | | | | | | | | | | | | |
 Db 660 -GGPEPPPSKDGDAVQTPQLYTTFLPPPEGVPPP-----ELACLPTPESTPELPV 709
 Qy 767 KRKPSRGSREWERNQN LINACTKDMPPMGSPVIPTDPLPLRASPSh----IPSVVVLPI 821
 | : | || || | | | | | | | | | | | | | | | |
 Db 710 KHLRAAGD-PWEWNQN RNNA-----KEPGGRSRGGHAAGGPAPRVLVRP-- 752
 Qy 822 QQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHL---SSKSPN HGVNLVENLDS- 876
 | | | | | | | | | | | | | | | | | | | | | |
 Db 753 -----PPPGCPGQ-----AVEVTTLEELLRYLHGPQPPRKGAEP PAPLTSR 793
 Qy 877 -LPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLK 935
 |||: | || | | : | | | | | | | | | | | | | |
 Db 794 ALPPE--PAPALLGGPSPRPHECASPLRLDV-----PPEGRCA SAPA--- 833
 Qy 936 RNNTNSSNSSHL---SRNQSFGRGDNP PAPQRVDSIQVHSSQPSQAVTVSRQPS-- 988
 | : | | | | | | | | | | | | | | | | | | | |
 Db 834 -RPALSAPAPRLGVGGGRRLPFSGHRAP PALLTRV-----PSGGPSRYSGGPGKHL 883
 Qy 989 --LNAYNSL TRSGLKRTPSLKP DVPPKPSF-APLSTMKPN 1026
 | | | | | | | | | | | | | | | | | | | | | |
 Db 884 LYLG RPEGYRGRALKRVDVEKPQQLSKPLVGPSRQAVPN 924

RESULT 7

US-09-254-594-3

; Sequence 3, Application US/09254594
 ; Patent No. 6566094
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMURA, Toru
 ; APPLICANT: KIKUCHI, Kaoru
 ; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
 ; FILE REFERENCE: 0020-4527P
 ; CURRENT APPLICATION NUMBER: US/09/254,594
 ; CURRENT FILING DATE: 1999-05-11
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 929

```

; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Tissue Type: Brain
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-3

Query Match           26.2%;  Score 1428.5;  DB 4;  Length 929;
Best Local Similarity 34.0%;  Pred. No. 1.5e-126;
Matches 360;  Conservative 147;  Mismatches 355;  Indels 197;  Gaps 32;

Qy      6 LLLYFTLLHFAGAGFPEDSEPIISISHGNYTKQYPVFGHKPGRNTTQRHRLDIQMIMIMN 65
Db      11 LLLLLLSSLPOAQATFPQDPPIPLLTSDLQGTSPSSWFRGLEDDAVAAEL-GLDFQRFLTLN 69

Qy      66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSROADVDTCRMKGKHDECHNFIKVL 124
Db      70 RTLLVAARDHVFSFDLQAQEEGEGLVPKFLTWRSQ--DMENCAVRGKLTDECYNYIRVL 127

Qy      125 LKKNDDALFVCGTNAFNPSERNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYS 184
Db      128 VPWDSQTLLACGTNSFSPVCRSYGITSLQQEGERSGQARCPFDATQSTVAISAEGLYS 187

Qy      185 ATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVEYN 244
Db      188 ATAADFQASDAVVYRSLGPQPPLRSAKYDSKWLREPHFVYALEHGDHVYFFLPEKSL-WR 246

Qy      245 T--MGKVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHYFNILQAVTDV 302
Db      247 TPGLGRVQFSRVARVCKRDMGGSPRALDRHWTSQLKRLNCSVPGDSTFYFDVLQLSTGP 306

Qy      303 IRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVP 362
Db      307 VNLHGRSALFGVFTTQTNSIPGSAVCAFYLDIERGFEKGKFEQRSLDGAWTPVSEDKVP 366

Qy      363 KPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTK 422
Db      367 SPRPGSCAGVGAALFSSSQDLPDDVLLFIKAHPLLPAVPPATHQP-LLTLSRALLTQ 425

Qy      423 IAVDTAAGPYQNHTVFLGSEKGIIILKFLARIGNSGFLNDSLFLLEMSVNSEKCSYDG 482
Db      426 VAVDGMAGPHRNTTVLFLGSNDGTVLKVLPP-GGQSLGPEPIILEEIDAYSHARCS--GK 482

Qy      483 ED----KRIMGMQLDRASSSLYVAFSTCVIKVPLGRERHGKCKKTCIASRDPYCGWIKE 538
Db      483 RSPRAARRIIGLELDTEGHRLFVAFPGCIVYLSRCARHGACQRSCLASLDPYCGWHRF 542

Qy      539 GGACSHLSPNSRLTFEQDIE-RGNTDGL--GDCHNSFVALNGHSSLLPSTTSDSTAQE 595
Db      543 RGCVNIRGPGG----TDVDLTGNQESMEHGDCQDG-----ATGSQSGPGDS 584

Qy      596 GYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLIKGHQDQLVPVTLLIAV 655

```

Db 585 AY-----GVRRDLSPASASRSIPIPLLLACV 610
 Qy 656 ILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGLFGDTQSK 715
 || :|| ||: || | || || : :| :||:: :| :|| :||
 Db 611 AAAFALGASVSGLLVSCAC--RRAN---RRRSKDIETPGLPRPLSLRSLARLHGGGPEP 664
 Qy 716 DPKP---EAILTPLMHNGKLATPGNTAKMLIKADQHHLTLALPTPESTPTLQQKRKPSR 772
 | | :| || :: | | | : :| || |||:|| | | :|
 Db 665 PPPPKDGDAAQTPQLYTTFLPPPEGGSPP-----ELACLPTPETTPELPVKHLRAS 715
 Qy 773 GSREWERNQNLIINACTKDMPPMGSPIPTDLP---LRASPSHIPSVVVLPIQQ---GYQ 826
 | | || ||| || | | | :| | | | | | :| |
 Db 716 GG-PWEWNQNQNNASEGPGRPRGCSAAGGPAPRVLVRPPPGCPGQEVEVTTLEELLRYL 774
 Qy 827 H-----EYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV 871
 | :| | :| || | | | || |
 Db 775 HGPQPPRKGSSEPLASAPFTSRPPASEPGAALFVD-----SSPMPR----- 814
 Qy 872 ENLDSSLPP-----KVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSY 920
 | :|| | :| | | | :| :|| :|
 Db 815 ---DCVPPLRLDVPPDGKRAAPSGRPALSAPAPRLGVSG-SRRL-----PF 856
 Qy 921 PTNSLTRSHQATTLKRNNTNSSNSHLSRNQSFGRGDNPAPPAPQRVDS--IQVHSSQPSG 978
 || | :| | | | :| |
 Db 857 PT-----HRA-----PPGLLTRVPSGGPSRYSGGPGR 883
 Qy 979 QAVTVSRQPSLNAYNSLTRGLKRTPSLKPDV--PPKPS 1015
 : :| | : | | | :| | || :| :||:
 Db 884 HLLYLGR-PDGHRGRSLKRVDVKSPLSPKPLATPPQPA 921

RESULT 8

US-09-653-274-10

```

; Sequence 10, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides
; FILE REFERENCE: HYS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-653-274-10

```

Query Match 25.3%; Score 1377.5; DB 4; Length 536;
 Best Local Similarity 49.3%; Pred. No. 4.1e-122;
 Matches 265; Conservative 97; Mismatches 167; Indels 9; Gaps 7;

 Qy 6 LLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFGHKPGRNTTQRHRLDIQMIMIMN 65
 ||| :|| | ||::| |:|| | | | | : | ||| : :||| : :|||
 Db 4 LLLLSSLPH-TQAAFPQDPLPLLISDLQGTSPLSWFRGLEDDAVAAEL-GLDFQRFLT 61

 Qy 66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSQRADVDTCRMKGKHDECHNFIKVL 124
 || :|||||::|:| : | : | ||::|: | |: | ::|| | ||::|:||:|||
 Db 62 RTLLVAARDHVFSFDLQAEEEGLVNPKYLTWRSQ--DVENCAVRGKLTDECYNYIRVL 119

 Qy 125 LKKNDDALFVCGTNAFPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYS 184
 : : | ||::|:| ||::| : :|: | :|| | ||::|| :||::|:| |||
 Db 120 VPWDSQTLLACGTNSFSPVCRSYGITSLQQEGEELSGQARCPFDATQSNVAIFAEGSLYS 179

 Qy 185 ATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVEYN 244
 || | | | ||::|:|||| | ||: | :|||||:||:||||::||:|||||:|||
 Db 180 ATAADFQASDAVVYRSLGPQPPLRSAKYDSKWLREPHFVQALEHGDHVYFFFREVSVEDA 239

 Qy 245 TMGKVVFPRAVQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDHSFYFNILQAVTDVIR 304
 :||| | ||::|:||| | |||| | |::| ||||||| ||||||| |||::|:||| :
 Db 240 RLGKVQFSRVARVCKRDGGSPRALDRHWTSDLKLRLNCVPGDSTFYFDVLQALTGPVN 299

 Qy 305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTVPVDERVPKP 364
 ::||| : |:| | |||||||: :|:| | |:|||:| | | ||| :||| |
 Db 300 LHGRSALFGVFTTQTNSIPGSAVCAFYLDEIERGFEGKFKEQRSLDGAWTPVSEDRVPSP 359

 Qy 365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA 424
 ||| ||| :||| :| ||| | ||| |||:| ||| :||| | | | |||:
 Db 360 RPGSCAGVGGAAALFSSSRDLPDDVLTIFIKAHPLLDPAVPPVTHQP-LLTTSRALLTQVA 418

 Qy 425 VDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVED 484
 || | ||: | ||::|:|| | :|| | | || : | ||: | :|| |
 Db 419 VDGMAGPHSNITVMFLGSNDGTVLKVLTGGRSGG-PEPILLEEIDAYS PARCSGKRTAQ 477

 Qy 485 --KRIMGMQLDRASSSLYVAFSTCVIKVPLGRCRERHGKCKKTCIASRDPYCGWIKEGG 540
 :|||:||| | :||| | :|: :|| | | || | :|||:|||:||| |
 Db 478 TARRIIGLELDTEGHRLFVAFSGCIVYLPLSRCARHGACQRSCLASQDPYCGWHSSRG 535

RESULT 9

US-08-121-713D-58
 ; Sequence 58, Application US/08121713D
 ; Patent No. 5639856
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; APPLICANT: Kolodkin, Alex L.
 ; APPLICANT: Matthes, David
 ; APPLICANT: Bentley, David R.
 ; APPLICANT: O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200

CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-121-713D-58

Query Match 17.8%; Score 969.5; DB 1; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

Qy 8 LYFTLLHFAGAGFPEDSEPISHGNYTKQYPVFVGHKPGRNTTQR-----HRLDIQMI 61
 | : || | : | | | | | | | | | | | : :::
 Pb 11 LIWVAIH--AAAWYNDVSP-----KMYVOE-----GEERVORFLGNESHKDHEKLI 54

Qy 62 MIMNGTLYIAARDHITYVDID--TSHTEEIYCSKKLTWKSROADVDTCRMKGKHDECHN 119
 : : | : ||: : | : | | : | : | : | : ||| :|| |
Pb 55 EKDHNLSILVGARNIVYNSLBDLTFETEO---RLEWHSSCAHRELCKYLCKKSEDDCON 109

Qy 120 FIKVLLKKNDDALFVCGTNAFNPSRCRNYKMDTLEPFGD----EFSGMARCYPDAKHANV 174
.:|:|| | :|| : :|||||: | |||: | : | | | : | | : | : | : | : | : | : | :
Ei 120 FIKVLLKKNDDALFVCGTNAFNPSRCRNYKMDTLEPFGD----EFSGMARCYPDAKHANV 174

Qy 175 ALFADGKLYSATVTDLAI DAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYF 234
|: :: : |: ||| || | : ||| ||| : | | | | || | : | | :|

Qy 235 FFREIAVEYNTMGKVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFN 294

Qy 295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPD 350

BB 260 ETQSTISDTIEGNTGGQVERLTIGVFTTIVNSIGGSAVCATSRKSTLEESTPDGTREQELEM 335

Qy 351 STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
| | || :||:|||| | | || ::||:|| |||||||: |||
Db 340 SNWLAVPSLKVPEPRPGQCVDND-----SRTLPDVSVNFVKSHTLMDEAVPAFFTRPI 391

Qy 411 FLRTMVRYRLTKIAVD---TAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLN---- 461
:| ::|| ||||| | | : :||:||:: | ::| | || :
Db 392 LIRISLQYRFTKIAVDQQVRTPDG--KAYDVLFIGTDDGKVIKAL---NSASFDSSTV 445

Qy 462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG 519
||: :||: | || | : ::|| | || | :: : | || ::
Db 446 DSVVIEELQVLP-----PGVPVKNLVYVRMDGDDSKLVVSDDEILAIKLHRCGSDKIT 499

Qy 520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN--SRLTFEQDIERGNTDGLGDCHNSFVAL 575
|:: |:: :||| | | : | |: : | :|| | | : :
Db 500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy 576 NGHSSSLPSTTSDSTA-----QEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNC 628
| | :|: | : | : | : | : :| : || : ||
Db 558 ---ASPVPTQPTTKSSGDPVHSIHQAEEFEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy 629 DKKGVIRESYLKGHDLVPV---TL-LAI-----AVILAFVMGAVFS 666
| | :|: | : | :|| | ::| | : | :||
Db 611 GSK-----LPSSQEKLPIYTAELTIAIVTSCLGALVVGFIISGFLFS 652

RESULT 10

US-08-835-268-58

; Sequence 58, Application US/08835268

; Patent No. 5807826

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,268

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713

; FILING DATE: 13-SEP-1993

; ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-835-268-58

Db 500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557
Qy 576 NGHSSLLPSTTSSTA-----QEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNC 628
Db 558 ---ASPVPTQPTTKSSGDPVHSIHQAEEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610
Qy 629 DKKGVIRESYLKGHQLVPV---TL-LAI-----AVILAFVMGAVFS 666
Db 611 GSK-----LPSSQEKLPIYTAETLTIAIVTSCIGALVVGFIISGFLFS 652

RESULT 11

US-09-060-692-58

; Sequence 58, Application US/09060692
; Patent No. 5935865
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,692
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-060-692-58

RESULT 12

US-08-833-391-58

; Sequence 58, Application US/08833391

; Patent No. 6013781
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,391
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-833-391-58

Query Match 17.8%; Score 969.5; DB 3; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

Qy 8 LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQR-----HRLDIQMI 61
| : || | : | | | | | | || | : ::
Db 11 LLWVALH--AAAWVNDVSP-----KMYVQF----GEERVQRFLGNESHKDHFKLL 54

Qy 62 MIMNGTLYIAARDHIYTVDID--TSHTEEIYCSKKLTWKSQRADVDTCRMKGKHKECHN 119
: : | : ||: :| : | | | : | : || : | :|| | :| :| |
Db 55 EKDHNSSLVGARNIVYNISLRDLTEFTEQ----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Qy 120 FIKVLLKKNDDALFVCGTNAFPSCRNPKMDTLEPFGD-----EFSGMARCPYDAKHANV 174

Db	110	YIRVLAKIDDRVLICGTNAYKPLCRHYALKD---GDYVVEKEYEGRGLCPFDPDHNST	165
Qy	175	ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHD SKWLKEPYFVQAVDYGDYIYF	234
Db	166	ATYSEGQLYSATVADFSGTDP LIYRG----PLRTERSDLKQLNAPNFVN TMEYNDIFF	220
Qy	235	FFREIAVEYNTMGKVVFP RVAQVCKNDMGG SQRVLEKQWTSFLKARLNCSVP GD SHFYFN	294
Db	221	FFRET AVEYINC GKAIYSRVARVCKHD KGGPHQGGDR-WTSFLKSRLNCSVP GDYP F YFN	279
Qy	295	IILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGS AVCAYDMLDIASVFTGRFKEQKSPD	350
Db	280	EIQSTS DII EGN YGGQ VKEKL IYGVFTT PVNSIGGSAVCAFS M KSILESFDGP F KEQETMN	339
Qy	351	STWTPV PDER VP KPRPGCCAGSS LERYATSNEFPDDTLNFIKTHPLMDEA VPSIFNRPW	410
Db	340	SNWLAVPSL KVPEPRPGQC VND-----SRTLPDV SVNFVKSH TLMD EA VPAFFTRPI	391
Qy	411	FLRTMVR YRLTKIAVD---TAAGPYQNHTVVFLGSEKG IILKFLARIGNSGFLN-----	461
Db	392	LIRISLQYRFTKIAVDQQV RTPDG--KAYDVLFIGTDDGKV IKA L---NSASF DSSDTV	445
Qy	462	DLSFLEEMS VYNSEKCSYDGVEDKRIMGMQLDRASS SLYVAFSTCVIKVPLGRC--ERHG	519
Db	446	DSV VIEELQVLP-----PGVPVKNLYVVRMDGDDSKLV VSD DEILAIK LHRC GSD KIT	499
Qy	520	KCKKTCIASRD PYCGWIKEGGAC SHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL	575
Db	500	NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLG EHKAC GGRP QTEIV-	557
Qy	576	NGHSSSLLPSTT SDSTA-----QEGYESRGGM LDWKHLLDSPDSTDPLGAVSSH NHQ	628
Db	558	----ASPVPTQPTT KSSGDPVHSI HQAEFEPE--IDNEIVIGVDDSNVI PNTLAEINHA	610
Qy	629	DKKGVIRESYLKGHDQLVPV---TL-LAI-----AVILA FVMGAVFS	666
Db	611	GSK-----LPS SOEKLP IYTAETLTIAIVT SCL GALVVGFI SGFLFS	652

RESULT 13

US-09-060-610-58

; Sequence 58, Application US/09060610

Patent No. 6344544

GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.

APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Tim

; TITLE OF INVENTION: The Semaphorin Gene Fam

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; 1000 PENNSYLVANIA AVENUE, N.W.
; WASHINGTON, D.C. 20004

; STREET: 268 Bush St.

; CITY: San Francisco
STATE: CA

; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,610
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,268
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-060-610-58

Query Match 17.8%; Score 969.5; DB 4; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

Qy 8 LYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQR-----HRLDIOMI 61
| : || | : | | | | | | | || | : :::
Db 11 LLWVALH--AAAWVNDVSP-----KMYVQF----GEERVQRFIGNESHKDHFKLL 54

Qy 62 MIMNGTLYIAARDHIYTV DID--TSHTEEIYCSKKLTWKS RQADVDTCRMKGHKDECHN 119
: : | : || : | : | | : | | | | : | : || | : | : | |
Db 55 EKDHNSSLVGARNIVYNISLRDLTEFTEQ----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Qy 120 FIKVLLKKNDALFVCGTNANPNSCRNYKMDTLEPFGD----EFSGMARC PYDAKHANV 174
: | : || | : | : | : | | : | | | | | : | | : | | : |
Db 110 YIRVLAKIDDRVLICGTNAYKPLCRHYALKD---GDYVVEKEYEGRGLCPFDPHNST 165

Qy 175 ALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHD SKWLKEPYFVQAVDYGDYIYF 234
| : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 166 AIYSEGQLYSATVADFSGTDPLIYRG----PLRTERSDLKQLNAPNFVNTMEYNDIFF 220

Qy 235 FFREIAVEYNTMGKV VPRVAQVCKNDMGGSQ RVLEKQWTSFLKARLNCSVPGD SHFYFN 294
| | | | | | | | : | : | : | : | : | : | : | : | : | : |
Db 221 FFRETA VEYINCGKAIYSRV ARVCKHDKGPHQGGDR-WTSFLKSRLNC SVP GDYD PFYFN 279

Qy 295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGS AVCAYDMLDIASVFTGRFKEQKSPD 350
: | : | : | | | | : | : | | | | | | | | | | | | | | : |
Db 280 EI QSTS DII EGNYGGQVEKLIYGVFTTPVNSIGGS AVCAF S MKS ILES FDGP FKEQETMN 339

Qy 351 STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
| | || :||:|||| | | :|| ::||:||:| |||||:| ||
Db 340 SNWLAVPSLKVPEPRPGQCVD-----SRTLPDVSVNFVKSHTLMDEAVPAFFTRPI 391

Qy 411 FLRTMVRYRLTKIAVD---TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN---- 461
:| ::|| ||||| | | : :||:||:| :|| | || :
Db 392 LIRISLQYRFTKIAVDQQVRTPDG--KAYDVLFIGTDDGKVIKAL---NSASFDSSTV 445

Qy 462 DSDLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYAFSTCVIKVPLGRC--ERHG 519
||: :||: | || | : ::| | | | : : | || :
Db 446 DSVVIEELQVLP-----PGVPVKNLYVVVRMDGDDSKLVVSDDEILAIKLHRCGSDKIT 499

Qy 520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL 575
| :| :||| | | :||: :| ||:| | | : :
Db 500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Qy 576 NGHSSLLPSTTSDDSTA-----QEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNC 628
:| :|: | :|: | :| :| : :|| :|| :||
Db 558 ----ASPVPTQPTTKSSGDPVHSIHQAEEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610

Qy 629 DKKGVIRESYLGHDQLVPV---TL-LAI-----AVILAFVMGAVFS 666
| | :|: || :|| |::: |: | :||
Db 611 GSK-----LPSSQEKLPIYTAETLTIAIVTSCLGALVGFISGFLFS 652

RESULT 14

PCT-US94-10151A-58

; Sequence 58, Application PC/TUS9410151A

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/10151A

; FILING DATE: 13-SEP-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299 FHT UR

; INFORMATION FOR SEQ ID NO: 58:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 730 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
PCT-US94-10151A-58

Query Match 17.8%; Score 969.5; DB 5; Length 730;
Best Local Similarity 34.4%; Pred. No. 5.7e-83;
Matches 244; Conservative 124; Mismatches 224; Indels 117; Gaps 29;

Db 11 LLWVALH--AAAWVNDVSP-----KMYVQF----GEERVQRFLGNESHKDHFKLL 54

Qy 62 MIMNGTLYIAARDHITYVDID--TSHTEEIYCSKKLTWKSROQADVDTCRMKGKHKDECHN 119
: : | : ||: : | : : | | : : | | | | : | : ||| : |||

Db 55 EKDHNSLLVGARNIVYNISRLDLTEFTEQ----RIEWHSSGAHRELCYLKGKSEDDCQN 109

Db 110 YIRVLAKIDDDRVLICGTNAYKPLCRHYALKD---GDYVVEKEYEGRGLCPFPDHNST 165

QY 175 ALFADGKLYSATVTDLAI DAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYF 234
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Pb 166 NYXECOL YGNTWTR DESCTPRLIVYGC RI PTERSGI KOLN VPUVETMVEVPEVPE 220

DB 166 AIYSEGQLYSATVADFSGTDPLIYRG----PLRTERSDLKQLNAPNFVNTMEYNDIFF 220

QY 235 FFRETAVEYNTMGKVFPRVAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFN 294
 ||||| ||| :: : ||::|||: || | : : :: ||||||:||||| |||||
 Pb 221 FFERETAVEYNCGKATYSPRVARVCKHDKGKGGPHOGGDP-WTSFLKSPRLNCSVPGDYPFEN 279

221 FFRETAVETINCGRATTSVARVCRHDKGGFRQGGDR-WI5FERSKRNCSVPGDTPPIEN 279

200 EQUISIDTECHNICSVEREITIIVYIIVVNSIGGSAVCAI SMRSTEESTPDT PREQETPAI 333

Db 340 SNWLAVPSLKVPEPRPGQCVND-----SRTLPDVSVNFVKSHTLMDEAVPAFFTRPI 391

Db 392 LIRISLQYRFTKIAVDQQVRTPDG--KAYDVLFIGTDDGKV1KAL---NSASFDSSTDV 445

Db 446 DSVVIEELQVLP-----PGVPVKNLYVVRMDGDDSKLVVVSDEILAIKLHRCGSDKIT 499

Db 500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557

Db 558 ----ASPVPTQPTTKSSGDPVHSIHQAEEPE---IDNEIVIGVDDSNVPNTLAEINHA 610

Db | : :|: || :|| |::: |: | :||
611 GSK-----LPSSQEKLPIYTAELTIAIVTSCLGALVVGFISGFLFS 652

RESULT 15

US-08-121-713D-60

; Sequence 60, Application US/08121713D

; Patent No. 5639856

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713D

; FILING DATE: 13-SEP-1993

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: B94-002-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415)343-4341

; TELEFAX: (415) 343-4342

; TELEX:

; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 650 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-121-713D-60

Query Match 16.1%; Score 880; DB 1; Length 650;

Best Local Similarity 35.8%; Pred. No. 1.6e-74;

Matches 207; Conservative 95; Mismatches 194; Indels 82; Gaps 19;

Qy 114 KDECHNFIKVLLKKNDALFVCGTNAFPNSCRNYKMD---TLEPPGDEFSGMARCPYDA 169
:|:| |:|:::: : |||||||:| | | | : ||| :| | | |

Db 1 EDDCQNYIRIMVVPSGPRLFVCGTNSFRPMNTYIISDSNYTLEA---TKNGQAVCPYDP 57

Qy 170 KHANVALFADGKLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYG 229

Db	58	RHNSTSVLADNELYSGTVADFSGSDPIIYRE-----PLQTEQYDSLSLNAPNFVSSFTQG	112
Qy	230	DYIYFFFREIAVEYNTMGKVVFPRTVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDS	289
Db	113	DFVYFFFRETAVEFINCGKAIYSRVARVCKWDKGPHR-FRNRWTSFLKSRLNCSIPGDY	171
Qy	290	HFYFNILQAVTDVIR----INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKE	345
Db	172	PFYFNEIQSASNLLVEQQYGMSSKLIYGVFNTPSNSIPGSAVCAFALQDIADTFEGQFKE	231
Qy	346	QKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSI	405
Db	232	QTGINSNWLPVNNAKVPDPGRPSC-----HNDRALPDPTLNFIKTHSLMDENVPAF	283
Qy	406	FNRPWFLRTMVRYRLTKIAVD---TAAGPYQNHTVVFLGSEKGIIILKFL-ARIGNSGFL	460
Db	284	FSQPILVRTSTIYRFTQIAVDAQIKTPGG--KTYDVIFVGTDHGKIIKSVNAESADSADK	341
Qy	461	NDSLFLLEMSVYNSEKCSYDGVEDKRIM-GMQLDRASSSLY-----VAFSTCVIKVPLG	513
Db	342	VTSVVIIEIDVLTKS---EPIRNLEIVRTMQYDQPKDGSYDDGKLIIVTDSQVVAIQLH	397
Qy	514	RC--ERHGKCKKTCIASRDPYCGWIKEGGAC-SHLSPN--SRLTFEQDIERGNTDGLGDC	568
Db	398	RCHNDKITSCSE-CVALQDPYCAWDKIAGKCRSHGAPRWLEENYFYQNVATGQ-----	449
Qy	569	HNSFVALNGHSSLLPSTTSSTAQEYESRGMLDWKHLLDSPDSTDPLGAVSSHNHQ	628
Db	450	-----HAACPSGKINSKDANAGEQKGFRNDM---DLLDS-----RRQ	483
Qy	629	DKKGVIRESYLKGHDQLPVVTLLAIAVILAFAVMGAVFS	666
Db	484	SKDQEIIDNIKDNFEDIINAQYTETLVMAVLAGSIFS	521

Search completed: March 24, 2004, 13:17:59
 Job time : 36.7132 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 24, 2004, 13:11:23 ; Search time 30.8439 Seconds
(without alignments)
3212.214 Million cell updates/sec

Title: US-09-856-681A-2

Perfect score: 5450

Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTS MKPNDACT 1030

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	971.5	17.8	730	2	JH0798	fasciclin IV precu
2	875	16.1	656	2	B49423	semaphorin I - fru
3	852.5	15.6	771	2	D49423	semaphorin III pre
4	845.5	15.5	711	2	A49423	semaphorin I precu
5	842.5	15.5	772	2	I48747	semaphorin D - mou
6	839.5	15.4	772	2	A49069	collapsin - chicke
7	830	15.2	1074	2	JC5928	semaphorin F precu
8	826	15.2	749	2	G01856	semaphorin V - hum
9	803	14.7	748	2	I48744	semaphorin A - mou
10	793.5	14.6	666	2	I58169	semaphorin III - m
11	789	14.5	712	2	T27165	hypothetical prote
12	779.5	14.3	724	2	C49423	semaphorin II prec
13	768	14.1	753	2	G02173	semaphorin III fam

14	737	13.5	751	2	I48748	semaphorin E - mou
15	692	12.7	834	2	S66498	M-sema F protein p
16	656	12.0	782	2	I48746	semaphorin C - mou
17	641.5	11.8	760	2	I48745	semaphorin B - mou
18	356.5	6.5	653	2	T03102	semaphorin homolog
19	322.5	5.9	676	2	T33853	hypothetical prote
20	238	4.4	1945	2	T13937	plexin A - fruit f
21	217	4.0	403	2	E42521	A39R protein - vac
22	208	3.8	441	2	S29921	hypothetical prote
23	199.5	3.7	1884	2	JC4975	plexin 2 precursor
24	182	3.3	1905	2	I51553	Plexin - African c
25	163.5	3.0	3968	2	A44265	trithorax homolog
26	158	2.9	2051	2	T13164	plexin B - fruit f
27	155.5	2.9	1894	2	JC4980	plexin 1 precursor
28	155	2.8	1375	1	JC5148	hepatocyte growth
29	155	2.8	2352	2	T30201	Notch homolog prot
30	153	2.8	625	2	S48941	regulatory protein
31	147.5	2.7	3507	2	T34513	hypothetical prote
32	147	2.7	1425	2	T30811	hepatocyte growth
33	146.5	2.7	295	2	JQ1775	Sall9R protein - v
34	140	2.6	1390	1	TVHUME	hepatocyte growth
35	139.5	2.6	3869	2	A48205	All-1 protein +GTE
36	138.5	2.5	1065	2	S19482	hypothetical prote
37	138	2.5	728	2	S48569	hypothetical prote
38	137	2.5	867	2	T41308	hypothetical zinc-
39	137	2.5	2492	1	C44213	nonstructural poly
40	136.5	2.5	1347	2	T02214	ubiquitous TPR mot
41	136	2.5	1310	2	T40135	oxysterol-binding
42	136	2.5	2531	2	S18188	notch protein homo
43	133.5	2.4	1829	2	T14280	RW1 protein - mous
44	133.5	2.4	2187	2	T30826	nascent polypeptid
45	133.5	2.4	2531	2	A46019	notch-1 protein -

ALIGNMENTS

RESULT 1

JH0798

fasciclin IV precursor - American bird grasshopper

C;Species: Schistocerca americana (American bird grasshopper)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: JH0798

R;Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Goodman, C.S.

Neuron 9, 831-845, 1992

A;Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in the grasshopper embryo.

A;Reference number: JH0798; MUID:93040225; PMID:1418998

A;Accession: JH0798

A;Molecule type: mRNA

A;Residues: 1-730 <KOL>

A;Cross-references: GB:L00709; NID:g160844; PID:g160845

A;Experimental source: embryo

C;Comment: This protein plays a role in growth cone guidance in the developing central nervous system.

C;Keywords: glycoprotein; transmembrane protein

| : : || : || :: | : | : ||
Db 611 GSK-----LPSSQEKLPIYTAETLTIAIVTSLGALVVGFIISGFLFS 652

RESULT 2

B49423

semaphorin I - fruit fly (*Drosophila melanogaster*) (fragment)

C;Species: *Drosophila melanogaster*

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999

C;Accession: B49423

R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules.

A;Reference number: A49423; MUID:94094332; PMID:8269517

A;Accession: B49423

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-656 <KOL>

A;Cross-references: GB:L26082

C;Genetics:

A;Gene: semal

A;Cross-references: FlyBase:FBgn0011259

Query Match 16.1%; Score 875; DB 2; Length 656;
Best Local Similarity 35.6%; Pred. No. 1.4e-50;
Matches 208; Conservative 95; Mismatches 193; Indels 88; Gaps 20;

Qy 114 KDECHNFIKVLLKKNDDALFVCGTNAFPSCRNYKMD---TLEPFGDEFSGMARCPYDA 169
Db 1 EDDCQNYIRIMVVPSPGRLFVCGTNSFRPMNTYIISDSNYTLEA---TKNGQAVCPYDP 57

Qy 170 KHANVALFADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYG 229
Db 58 RHNSTSVLADNELYSGTVADFGSDPPIYRE----PLQTEQYDLSLSLNAPNFVSSFTQG 112

Qy 230 DYIYFFFREIAVEYNTMGKVVFPRAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDS 289
Db 113 DFVYFFFRETAVEFINCGKAIYSRVARVCKWDKGPHR-FRNRWTSFLKSRLNCIPGDY 171

Qy 290 HFYFNILQAVTDVIR---INGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKE 345
Db 172 PFYFNEIQSASNLEGQYGSMSKLIYGVFNTPSNSIPGSACAFALQDIADTFEGQFKE 231

Qy 346 QKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSI 405
Db 232 QTGINSNWLPVNNAKVPDPRGSC-----HNDSRALPDPTLNFIKTHSLMDENVPAF 283

Qy 406 FNRPWFLRTMVRYRLTKIAVD---TAAGPYQNHTVVFLGSEKGIILKFL-ARIGNSGFL 460
Db 284 FSQPILVRTSTIYRFTQIAVDAQIKTPGG--KTYDVIFVGTDHGKIIKSVNAESADSADK 341

Qy 461 NDSLFLLEEMSVYNSEKCSYDGVEDKRIM-GMQLDRASSSLY-----VAFSTCVIKVPLG 513
Db 342 VTSVVIIEIDVLTKS---EPIRNLEIVRTMQYDQPKDGSYDDGKLIIVTDSQVVAIQLH 397

Qy	514	RC--ERHGKCKKTCIASRDPYCGWIKEGGAC-SHLSPN--SRLTFEQDIERGNTDGLGDC	568
		:: : : : ::	
Db	398	RCHNDKITSCSE-CVALQDPYCAWDKIAGKCRSHGAPRWLEENYFYQNVATGQ-----	449
Qy	569	HNSFVALNGHSSSLPSTTSYSTAQEGYESRGGMULDWKHLLDSPDSTDPLGAVSSHNHQ	628
		:: : :	
Db	450	-----HAACPSGKINSKDANAGEGKGFRNDM---DLLDS-----RRQ	483
Qy	629	DKKGVIRESYLKGH-----QLVPVTLLAIAVILAFAVMGAVFS	666
		:: : :: :: : ::	
Db	484	SKDQEIIDNIDKNFEGPQTSADIINAQYTVELVMAVLAGSIFS	527

RESULT 3

D49423

semaphorin III precursor - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995

C;Accession: D49423

R; Kolodkin, A.L.; Matthe:

Cell 75, 1389-1399, 1993
A;Title: The Semaphorin genes encode a family of transmembrane and secreted

growth cone guidance molecules.

A; Reference number:

A;Accession: D49423

A; Status: preliminary.

A;Molecule type: mRNA

A;Residues: 1-771 <KOL> 0.0000 0.000 7000000 0.000000 0.000000 1 0.000000

A;Cross-ref

C; Genetics:

A;Gene: GDB:SEMA1

A; Cross-ref

C; Superfamily: semaphorin

Query Match 15.6%; Score 852.5; DB Z; Length 111;
 Best Local Similarity 32.1%; Pred. No. 5.8e-49;
 Matches 208; Conservative 106; Mismatches 250; Indels 83; Gaps 20;

Qy 44 HKPGRNTTQRHRLDIQMIMIMNGT-----LYIARDHIYTVD 80
:: | :| | :| : : :: | ||: | :||:: |

Db 22 YQNGKNNVPRLKSYKEMLESNNVITFNGLANSYYHTFLLDEERSRLYVGAKDHIFSFD 81

Qy 81 IDTSHTEEIYCSKKLTWKSROADVDTCRMKGKH-KDECHNFIKVLLKKNDALFVCGTNA 139
: | :|: | | | || ||| | | |:| | |

Db 82 L-----VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGA 136

Qy 140 FNPSCR-----NYKMDTLEPGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFA 192
| : | :: | : : || : || | : || | : || | | : | | | | | | | |

Db 137 FHPICTYIEIGHHPEDNIFKLLENSHFENGGRGKSPYDPKLLTASLLIDGELEYSGTAADFMG 196

Qy 193 IDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYIYFFREIAVEYNT 245
| |::|:|| :|| :||||:|| :| :| | :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 197 RDFAI FRTLGHHHPIRTEQHDSRWLNDPKFISAHЛИSESDNPEDDKVYFFFRENATDGEH 256

Qy 246 MGKVVPRVAQVKNDMGGSQRVLEKQWTSFLKARLNCSVPG---DSHFYFNILQAVTD 301
|| | : | : || || | | : || : || || | | | | | : || | : |

Db 257 SGKATHARIQQICKNDFGG-HRSLVNKWTTFLKARLICSVPGPNGIDTHF-----DELQD 310

Qy	302	VIRINGRD----VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPV	357
	: : : : : : : :		
Db	311	VFLMNFKDPKNPVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRGPNYQWVPY-	369
Qy	358	DERVPKPGRPCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR	417
	: : :: : : :		
Db	370	QGRVPYPRPGTCP-SKTFGGFDSTKDLPPDDVITFARSHPAMYNPVFPMMNNRPIVIKTDVN	428
Qy	418	YRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNSEKC	477
	: : : : :		
Db	429	YQFTQIVVDRVDAEDGQYDMFIGTDVGTVLKVVSIPKETWYDLEEVLLEEMTVFR----	484
Qy	478	SYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWI	537
	:		
Db	485	-----EPTAISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECLARDPYCAW--	537
Qy	538	EGGACSHLSPNS-RLTFEQDIERGNTDGLGDC---HNSFVALNGHS--SSLNPSTTSD	590
	: :		
Db	538	DGSACSRYFPTAKRTRRQDIRNG--DPLTHCSDLHHDNH---HGHSPEERIIYGVENSS	592
Qy	591	STAQEGBESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRES	637
	: : : : : : : :		
Db	593	TFLECSPKSQRALVYWFQFQRRNEERKEEI-RVDDHIIRTDQGLLLRS	638

RESULT 4

A49423

semaphorin I precursor - beetle (*Tribolium confusum*)

C; Species: *Tribolium confusum*

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999

C;Accession: A49423

R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules.

A; Reference number: A49423; MUID: 94094332; PMID: 8269517

A;Accession: A49423

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-711 <KOL>

A;Cross-references: GB:II

```

Query Match           15.5%;  Score 845.5;  DB 2;  Length 711;
Best Local Similarity 28.9%;  Pred. No. 1.5e-48;
Matches 230;  Conservative 130;  Mismatches 270;  Indels 165;  Gaps 30

Qy      12 LLHFAGAGFPEDSEPI----SISHGNYTKQYPVFVGHKPGRNNTTQRHRLDIQMIMIMN- 65
        |:   |  |: | :       |:  ::|          |  |  |          :::|
Db      12 LIALCHAWMPDSSSKLINHKSVESKSFT-----GNATFPDH-----FIVLNLQ 54

Qy      66 --GTLYIAARDHIYTVDI-DTSHTEEIYCSKKLTWKSRSQADVDTCRMKGKHDECHNFIK 122
        :: :  |: :| : | || | :       :: | |  |  | :|| | :| |:|:
Db      55 DETSILVGGGRNRVYNLNSIFDLSERK---GGRIDWPSSDAHGQLCILKGKTDDDCQNYIR 110

Qy      123 VLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGD-EFSGMARCPYDAKHANVALFADGK 181

```

Db	111	ILYSSEPGKLVICGTSYKPLCRTYAFKEGKYLVEKEVEGIGLCPYNPEHNSTSVDQSYNGQ	170
Qy	182	LYSATVTDLAI DAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAV	241
Db	171	LFSATVADFSGGDPLIYRE----PQRTELSDLKQLNAPNFVN S VAYGDYI FFFYRETAV	225
Qy	242	EYNTMGKVVFPRVAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTD	301
Db	226	EYMNCGVYIYSRVARVCKDDKGPHQS RDR-WTSFLKARLNCSIPGEYPFYFDEIQSTSD	284
Qy	302	VI--RINGRD--VVLATFSTPYNSIPGSAVCAYDM LDIASVFTGRFKEQKSPDSTWTPVP	357
Db	285	IVEGRYNSDDS KIIYGILTPVNAIGGSAICAYQMADILRVFEGSFKHQETINSNWLPVP	344
Qy	358	DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFRLTMVR	417
Db	345	QNLVPEPRPGQCVRDSRI-----LPDKNVNFIKTHSLMED-VPALFGKPVLVRVSLQ	395
Qy	418	YRLTKIAVDTAAGPYQNH--TVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSE	475
Db	396	YRFTA ITVDPQVKTI NNQYLDVLYIGTDDGKV LK-----	429
Qy	476	KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCV-----IKVP-----	511
Db	430	-----AVNIPKRHAKALLYRKYRTSVPHGAPVKQLKIA PGYGVVVVGKDEIR	478
Qy	512	--LGR CERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLTF-EQDIERGN-----	561
Db	479	LANLNHCASKTRC-KDCVELQDPHC AWDAKQNLCVSIDTVTSYRF LIQDV VRGDDNK CWS	537
Qy	562	--TDGLGDCHNSFVALNGHSSSLPSTTS DSTAQE YESRGGM LDWKHLLD SPDSTDPL	619
Db	538	PQTDKKTVIKNK-----PSEVENEIT-----NSIDEKDL---DSSDPL	572
Qy	620	GAVSSHNNHQDKKGVIRESYLKG--HDQLVPVT--LLAIAVILA FVMGA---VFSGITVY	671
Db	573	IKTGLDDSDCDPV-SENSIGGC AVRQQLVIYTAGTLHIVVVVV SIVGLFSWLYSGLSVF	631
Qy	672	CV--CDHRRKDVAVVQRKE--KELTHSRRGSMS-SVTKL SGLFGDTQSKDPKPEA ILTPL	726
Db	632	AKFHSDSQYPEAPFIEQHNHLERLSANQTGYLT PRANKAVNLVVKVSSSTPRPKKDNL DV	691
Qy	727	MHNGKLATPGNTAKM 741	
Db	692	SKDLNIA SDGTLQK 706	

RESULT 5

148747

semaphorin D - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 24-Sep-1999

C;Accession: I48747

R; Puschel, A.W.; Adams, R.H.; Betz, H.

R,Fusco, A.W., Adams, P.
Neuron 14: 941-948. 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.
A;Reference number: I48744; MUID:95267431; PMID:7748561
A;Accession: I48747
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-772 <RES>
A;Cross-references: EMBL:X85993; NID:g854329; PIDN:CAA59985.1; PID:g854330
C;Genetics:
A;Gene: semD
C;Superfamily: semaphorin

Query Match 15.5%; Score 842.5; DB 2; Length 772;
Best Local Similarity 34.3%; Pred. No. 2.7e-48;
Matches 200; Conservative 85; Mismatches 225; Indels 73; Gaps 16;

Qy 47 GRNTTQRHRLDIQMIMIMNGT-----LYIAARDHIYTVDIDT 83
|:| . | :| : ::| |:|:||:: ::|
Db 25 GKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHIFS FNL-- 82

Qy 84 SHTEEIYCSKKLTWKS RQADVDTCRMKGKH-KDECHNFIKVLLKKNDDALFVC GTNAFNP 142
| :|:| :| | :| :|| ||| ||| | |:| ||| ||:|
Db 83 ---VNIKDFQKIVWPVS YTRRDECKWAGKDILKECANFIKVLEAYNQTHLYACGTGAFHP 139

Qy 143 SCR----NYKMDTLEPFGDEF--SGMARCPYDAKHANVALFADGKLYSATVTD FLAIDA 195
| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 140 ICTYIEVGHHPEDNIFKLQDSHFENG RGKSPYDPKLLTASLLIDGELYSGTAADFMGRDF 199

Qy 196 VIYRSLGESPTLRTVKHD SKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNTMGK 248
|:|:||:| :|| :||:|| :| |:| | :|:||| | :| :||
Db 200 AIFRTLGDHHPIRTEQHDSRWLNDPRFISAHLIPESDNPE DDKVYFFFRENAIGGEHSGK 259

Qy 249 VVFPRVAQVCKNDMGG SQRVLEKQWTSFLKARLNCSVPG---DSHFYFNILQAVTDVIR 304
|:| :|:||| | | :| :||:||||| | ||| | :||| :| :|||
Db 260 ATHARIGQICKND FGG-HRSLV NKWTTF LKARLIC SVPGP PNGIDTHF----DEL QDVFL 313

Qy 305 INGRD---VVLATFSTPYNSIPGS AVCAYDM LDIASVFTGRFKEQKSPD STWTPVP DER 360
|:| :| :| :| | | :| :| :| :| :| :| :| :| :| :|
Db 314 MNSKDPKNPIVYGVFTSSNIFKGSAVCMYMSDVRRVFLGPYAH RDGP NYQWVPY-QGR 372

Qy 361 VP KPRPGCCAGSSSLERYAT SNEFP DTLNF IKTHPLMDEA VPSIFNRPWFLRTMVRYRL 420
| | :||| | | :| :| :| :| :| :| :| :| :| :| :|
Db 373 VP YPRPGTCP-SKTFGGFDSTKDL PDDVITFGRSHPAMYNPVFPINNR PIMIKTDVN YQF 431

Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKG IILKFLARIGNSGFLNDSL FLEEMS VYNSEKCSYD 480
|:| | | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 432 TQIVVDRVDAEDGQYDVMFIGTDVGTVLKVSVPKETWHDLEEVL LEEMTVFR----- 484

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKT CIASRD PYCGWIKEGG 540
| | | :| | | :| :| :| :| :| :| :| :| :| :| :|
Db 485 --EPTTISAMELSTKQQQLYIGSTAGVAQLPLHRC DIYGKACAECCLARDPYCAW--DGS 540

Qy 541 ACSHLSPNS-RLT FEQDIERGNTDGLGDCHNSFVALNGHSSL 582
|:| | :| | :| | :| | :| | :| | :| | :|
Db 541 SCSRYFPTAKRRTRRQDIRNG--DPLTHCS DLEDHDNHHGPSL 581

RESULT 6
 A49069
 collapsin - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-1999
 C;Accession: A49069
 R;Luo, Y.; Raible, D.; Raper, J.A.
 Cell 75, 217-227, 1993
 A;Title: Collapsin: a protein in brain that induces the collapse and paralysis of neuronal growth cones.
 A;Reference number: A49069; MUID:94006554; PMID:8402908
 A;Accession: A49069
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-772 <LUO>
 A;Cross-references: GB:U02528; NID:g410078; PIDN: AAC59638.1; PID:g410079
 C;Superfamily: semaphorin

Query Match 15.4%; Score 839.5; DB 2; Length 772;
 Best Local Similarity 35.2%; Pred. No. 4.3e-48;
 Matches 198; Conservative 87; Mismatches 220; Indels 57; Gaps 17;

Qy	68 LYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRADVDTCRMKGKH-KDECHNFIKVLLK	126
	: :: :: :: : : :	
Db	69 LYVGAKDHIFSFLN----VNIKEYQKIVWPVSHSRRDECKWAGKDILRECANFIKVLLKT	123
Qy	127 KNDDALFVCGTNAFNPSR----NYKMDTLEPGDEF--SGMARCPYDAKHANVALFAD	179
	: : :: : : : :	
Db	124 YNQTHLYACGTGAFHPMCTYIEVGSHPEDNIFRMEDSHFENGGRGKSPYDPKLLTASLLVD	183
Qy	180 GKLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYI	232
	: : : : : : : :	
Db	184 GELYSGTAADFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPRFISAHLIPESDNPEDDKI	243
Qy	233 YFFFREIAVEYNTMGKVVFPRTVAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPG---D	288
	:: : : : : :	
Db	244 YFFFRENAIDGEHTGKATHARIQICKNDFGG-HRSLVNVKWTTFLKARLICSVPGPNGID	302
Qy	289 SHFYFNILQAVTDVIRINGRD---VVLATFSTPYNSIPGSACAYDMLDIASVFTGRFK	344
	: : : : : : :	
Db	303 THF----DELQDVFLMNSKDPKNPIVYGVFTTSSNIFKGSACVCMYSMTDVRRVFLGPYA	357
Qy	345 EQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPS	404
	: : : : : :	
Db	358 HRDGPNYQWVPPY-QGRVPYPRPGTCP-SKTFGGFDSTKDLPDEVITFARSHPAMNPVFP	415
Qy	405 IFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFGLSEKGIILKFLARIGNSGFLNDL	464
	: : : : : :	
Db	416 INSRPIMIKTDVDYQFTQIVVDRVDAEDGQYDVMFIGTDIGTVLKVVSIKPETWHEEEV	475
Qy	465 FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYAFSTCVIKVPLGRCERHGCKKT	524
	: : ::	
Db	476 LLEEMTVFR-----EPTVISAMKISTKQQQLYIGSATGVSQPLHRCDVYGKACAE	526
Qy	525 CIASRDPYCGWIKEGGACSHLSPNS-RLTFEQDIERGNTDGLGDCHNSFVALNGHSSLL	583
	: : : :	
Db	527 CCLARDPYCAW--DGSSCSRYFPTAKRRTRRQDIRNG--DPLTHCSD---LQHHDN---	575

QY 584 PSTTTSDSTAQEYESRGGMED 605
|| | : | | : |:
Db 576 PSGQTLEEKIIYGVENNSTFLE 597

RESULT 7

JC5928

semaphorin F precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 17-Nov-2000

C;Accession: JC5928

R;Simmons, A.D.; Pueschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M.
Biochem. Biophys. Res. Commun. 242, 685-691, 1998

A;Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-chat candidate interval.

A;Reference number: JC5928; MUID:98125554; PMID:9464278

A;Accession: JC5928

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1074 <SIM>

A;Cross-references: GB:U52840; NID:g2772583; PIDN: AAC09473.1; PID:g2772584

A;Experimental source: brain

C;Comment: This protein disrupts normal brain development and leads to some of the features of Cri-du-chat.

C;Genetics:

A;Gene: semaf

C;Superfamily: human semaphorin F; thrombospondin type 1 repeat homology

F;1-20/Domain: signal sequence #status predicted <SIG>

F;50-533/Domain: semaphorin #status predicted <SEM>

F;840-896/Domain: thrombospondin type 1 repeat homology <THR3>

F;971-993/Domain: transmembrane #status predicted <TMM>

Query Match 15.2%; Score 830; DB 2; Length 1074;
Best Local Similarity 36.2%; Pred. No. 3.1e-47;
Matches 199; Conservative 90; Mismatches 211; Indels 50; Gaps 17;

QY 68 LYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRADVDTCRMKGKHDECHNFIKVLLKK 127
| : ||::: : : |:: : : |: : | ||| |:|| |:|:|| |:
Db 70 LVVGARNYLFRQLQ-----EDLSLIQAVEWECDEATKKACYSKGSKKEECQNYIRVLL-V 123

QY 128 NDDALFVCGTNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALF-ADGKLYSAT 186
| || | ||||| | ||| : | | : ||||||| : | : || | | :||:|| |:
Db 124 GGDRLFTCGTNAFTPVCNRSLSNLAEIHDQISGMARCPYSPQHNSTALLTAGGELYAA 183

QY 187 VTDFLAIDAVIYRSLGESPTLRTVKHDSKWLEPYFVQAVDYGDIYFFFREIAVEYNTM 246
|| | | ||||| | ||| ::||| || || : | |: ||||| ||:: :
Db 184 AMDFPGRDPAIYRSLGLPPLRTAQYN SKWLNEPNFVSSYDIGNFTYFFFREN AVEHD-C 242

QY 247 GKVVFPRVAQVCKNDMGGSQLRKWLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRIN 306
| | | | |:|||:|| : | | : ||:|:||| ||| | |: | |: | : :
Db 243 GKTIVFSRAARVCKNDIGG-RFLLEDWTTFMKARLNCSRGEVPFYNNELQSTFFLPEL- 300

QY 307 GRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRP 366
|: | :| | ||| ::| | |:| | |: | | | |: | | |
Db 301 --DLIYGIFFT NVNSIAASAVCVFNL SAIAQAFSGPFKYQENSRSAWLPYPN--PNPHF 355

QY	367	GCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVD	426
	: : : :		
Db	356	QCGTVDQGLYVNLTERNL-QDAQKFILVH---EVVQPVTTVPSFMEDNSRF--SHVAVD	408
QY	427	TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFEEMSVYNSEKCSYDGVEDKR	486
	:: : : : : : : : :		
Db	409	VVQGREALVHIYLATDYGTIKKVRVPLNQT---SSSCLLEEIELFPERR-----REP	458
QY	487	IMGMQLDRASSSLYVAFSTCVIKVPLGRCRERHGKCKKTCIASRDPYCGWIKEGGACSHLS	546
	: : : : : : : : : : :		
Db	459	IRSLQILHSQSVLFVGRLREHVVKIPLKRCQFY-RTRSTCIGAQDPYCGWDVVMKKCTSLE	517
QY	547	PNSRLT-FEQDIERGNTDGLGDCHNSFVALNGHSSSLPST--TTSDSTAQEYESRGGM	603
	: : : : : : :		
Db	518	ESLSMTQWEQSISA-----CPTRNLTVDGHFGVWSWTPCTHTDGSAV-----GSC	563
QY	604	LDWKHLLDSP	613
Db	564	LCRTRSCDSP	573

RESULT 8

G01856

semaphorin V - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999

C;Accession: G01856

R;Sekido, Y.

submitted to the EMBL Data Library, June 1995

A;Reference number: G08634

A;Accession: G01856

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-749 <SEK>

A;Cross-references: EMBL:U28369; NID:g974283; PIDN:AAD09138.1; PID:g974284

C;Superfamily: semaphorin

Query Match 15.2%; Score 826; DB 2; Length 749;
 Best Local Similarity 34.7%; Pred. No. 3.3e-47;
 Matches 198; Conservative 88; Mismatches 228; Indels 56; Gaps 16;

Qy	66	GTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRADVDTCRMKGKH-KDECHNFIKVL	124
	:: : : : : : : : : : : : : : : : : : :		
Db	65	GRLFVGAENHVASLNLDNISKR---AKKLAWPAPVEWREECNWAGKDGTGECMNFKVLL	120
Qy	125	LKKNDDALFVCGTNAFNPSERNYKMD-----TLEPFGDEFSGMARCPYDAKHANVAL	176
	: : : : : : : : : : : : : : : : :		
Db	121	HAYNRTHLLACGTGAFHPTCAFVEVGHRAEPPVRLDP-GRIEDGKGKSPYDPRHRAASV	179
Qy	177	FADGKLYSATVTDLAIADAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAV-----DYG	229
	: : : : : : : : : : : : : : : : :		
Db	180	LVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWIINEPKFVKVFWIPESENPD	239
Qy	230	DYIYFFFREIAVE-YNTMGKVVFPRTVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSV--	286
	: : : : : : : : : : : : : : :		
Db	240	DKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGG-QRSILVNKWTTFLKARLVCSPGV	298

Qy	287	-GDSHFYFNILQAVTDVIRINGR-----VVLATFSTPYNSIPGSACVAYDMLDIASVFTG	341
	:	: :: :: : :	
Db	299	EGDTHF-----DQLQDVFLSSRDHRTPLLYAVFSTSSSIFQGSAVCVYSMNDVRRAFLG	353
Qy	342	RFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSLERYATSNEFPDDTLNFIKTHPLMDEA	401
	:: : ::: : : : :		
Db	354	PFAHKEGPMHQWVSY-QGRVPYPRPGMCP-SKTFGTFSSTKDFPDDVIQFARNHPLMYNS	411
Qy	402	VPSIFNRPWFLRTMVRYRLTKIAVDTAACGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLN	461
	: : : : : : :		
Db	412	VLPTGGRPLFLQVGANYFTQIAADRVAAADGHYDVLFIGTDVGTVLKVISVPKGSRPSA	471
Qy	462	DSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYAFSTCVIKVPLGRcerHGKC	521
	: : : : : : : : :: :		
Db	472	EGLLLEELHVFE-----DSAATVSMQISSKRHQLYVASRSAVAQIALHRCAAHGRV	522
Qy	522	KKTCIASRDPYCGWIKEGGACSHLSPNSRLTF-EQDIERGNTDGLGDCHNSFVALNGH--	578
	: : : : : :		
Db	523	CTECCLARDPYCAW--DGVACTRFQPSAKRRFRRQDVRNGDPSTLCSDSSRPALLEHKV	580
Qy	579	-----SSSLLPSTTTSSTAQEYESRGGM	603
	: :		
Db	581	FGVEGSSAFLECEPRSLQARVEWTFQRAGV	610

RESULT 9

I48744
semaphorin A - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I48744
R;Puschel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.
A;Reference number: I48744; MUID:95267431; PMID:7748561
A;Accession: I48744
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-748 <RES>
A;Cross-references: EMBL:X85990; NID:g854323; PIDN:CAA59982.1; PID:g854324
C;Genetics:
A;Gene: semA
C;Superfamily: semaphorin

```

Query Match           14.7%; Score 803; DB 2; Length 748;
Best Local Similarity 35.5%; Pred. No. 1.1e-45;
Matches 191; Conservative 80; Mismatches 205; Indels 62; Gaps 18;

Qy      66 GTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKS RQADVDTCRMKGKH-KDECHNFIKVL 124
        | |::| :|: ::| :||| | : :| || || |::| :
Db      65 GRLFVGAEHVASLSLDNISKR---AKKLAWPAPVEWREECNWAGKDGTGECMNFVRLL 120

Qy      125 LKKNDDALFVCGTNAFN PSCRNYKMDTL-----EPFGDEFSGMARCPYDAKHANVA 175
        | | | | |:|:| :| :| | | | | | :| | :| :
Db      121 HAYNHHTHLLACRTGAFHPTCALWRWATAGGTHASTGPEKLED---GKGKTPYDPRHRPPS 177

```

RESULT 10
I58169
semaphorin III - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999
C;Accession: I58169
R;Messersmith, E.K.; Leonardo, E.D.; Shatz, C.J.; Tessier-Lavigne, M.; Goodman, C.S.; Kolodkin, A.L.
Neuron 14, 949-959, 1995
A;Title: Semaphorin III can function as a selective chemorepellent to pattern sensory projections in the spinal cord.
A;Reference number: I58169; MUID:95267432; PMID:7748562
A;Accession: I58169
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-666 <RES>
A;Cross-references: GB:L40484; NID:g703189; PIDN:AAA73934.1; PID:g703190
C;Genetics:
A;Gene: SemaIII
C;Superfamily: semaphorin

Query Match 14.6%; Score 793.5; DB 2; Length 666;
Best Local Similarity 34.1%; Pred. No. 4.1e-45;
Matches 188; Conservative 89; Mismatches 226; Indels 49; Gaps 15;

Qy 116 ECHNF1KVLKKNDALFVCGTNAFPSCR----NYKMDTLEPGDEF--SGMARCPYD 168
|| |||||| | : ||| :: || | : | : | : | : | : |||
Db 7 ECANFIKVLEAYNOTHLYACGTGAFHPICTYIEVGHHPEDN1FKLODSHEFNGRKSPYD 66

Qy	169	AKHANVALFADGKLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQA---	225
	:	:	: : :
Db	67	PKLLTASLLIDGELYSGTAANFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPRFISAHLI	126
Qy	226	----VDYGDYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARL	281
	:	:	: :
Db	127	PESDNPEDDKVYFFFRENAIDGEHSGKATHARIGQICKNDFGG-HRSLVNVKTTFLKARL	185
Qy	282	NCSVPG---DSHFYFNILQAVTDVIRINGRD---VVLATFSTPYNSIPGSAVCAYDML	333
	:	: : :	: :
Db	186	ICSVPGPNGIDTHF---DELQDVFLMNSKDPKNPIVYGVFTTSSNIFKGSAVCYMSMS	240
Qy	334	DIASVFTGRFKEQKSPDSTWT PVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIK	393
: : :		: : : : :	
Db	241	DVRRVLLGPYAHRGPNYQWVPY-QGRVPYPRPGTCP-SKTEGGFDSTKDLPPDDVITFAR	298
Qy	394	THPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLAR	453
:	:	: : : : :	
Db	299	SHPAMYNPVFPINNRPIMIKTDVNYQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVSV	358
Qy	454	IGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLG	513
: :		: : :	
Db	359	PKETWHDLEEVLLEEMTVFR-----EPTTISAMELSTKQQQLYIGSTAGVAQLPLH	409
Qy	514	RCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNS-RLTFEQDIERGNTDGLGDCHNSF	572
:	:	: :	
Db	410	RCDIYKGACAECLARDPYCAW--DGSSCSRYPFTAKRRTRRQDIRNG--DPLTHCSDLQ	465
Qy	573	VALNGHSSL---LPSTTTSDSTAQEYESRGGMLDWKHLLDSPDSTDPLGAVSSHNNHQ	628
	:	: :	
Db	466	HHDNHHGPSLEERIYGVENSSTFLECSPKSQRALVYWFQRRNEDRKEEI-KMGDHIIIR	524
Qy	629	DKKGVIRESYLK 640	
:: ::			
Db	525	TEOGLLIJRSIOK 536	

RESULT 11

T27165

hypothetical protein Y54E5B.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 15-Oct-1999

C;Accession: T27165

R; Lennard, N.

submitted to the EMBL Data Library, October 1998

A; Reference number: Z20321

A;Accession: T27165

A;Status: preliminary; translated from GB/EMBL/DDBJ/T

A: Molecule type: DNA

A: Residues: 1-712 <W>

A:Cross-references: EMBL:AI032653; PTIDN:CAA21714 1;

A: Experimental sources

C: Genetics:

A:Gene: CESB;Y54E5B_1

A: Gene. CES
A: Man, positive

A, Map position: 1

A;Introns: 36/1; 70/2; 85/3; 194/2; 221/1; 253/3; 301/1; 352/3; 522/2; 560/1; 599/3; 655/3

Query Match 14.5%; Score 789; DB 2; Length 712;
Best Local Similarity 28.7%; Pred. No. 9.1e-45;
Matches 229; Conservative 129; Mismatches 282; Indels 158; Gaps 29;

Qy 6 LLLYFTLLLHFAGAGFPEDSEPIISHGNYTKQYP-----VFVGHKPGRNTTQRHRLDIQ 59
Db 7 LLLLNVV-----RSSEAIT---GGVVNLRPKQIINSVGIGDRFGGIGTSSDESDHF 55

Qy 60 MIMIMNG-TLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGKHKECH 118
Db 56 KLLAADGDSLLVGARNAVYNLSLST----LSVNHKIDWKPPAHEHIEECIMKGKSKTDCQ 110

Qy 119 NFIKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPFG---DEFSGMARCPTYDAKHANV 174
Db 111 NYIRVLARKSAGVSLVCGTHAFSPKCREY---TVTEFGIRNTRQFDGQGISPYDPKHNSS 167

Qy 175 ALFADG--KLYSATVTDFLAIDAVIYR-SLGESPT----LRTVKHDSKWLKEPYFVQA 225
Db 168 ALYVPGTNQLFVATVTDFVGNDALIYRKTIDETPSSKSAANIRTQSYDARVLNAPNFVAT 227

Qy 226 VDYGYIYFFFREIAVEY--NTMGKVVFPRAQVCKNDMGSQRVLEKQWTSFLKARLNC 283
Db 228 FAYKEHVFWFREIASEAINNEEPQIYARVARVCKNDKGGA-RPANERWTSYLKARLNC 286

Qy 284 SVP-GDSHFYFNILQAVTDVIRI-NGRDVVLATFSTPYNSIPGSACAYDMLDIASVF-T 340
Db 287 SLPSGSSPFYFNELKAVSDPIDAGNNHVYTFSTPDSDVRMSAVCKFSMKKIREFDN 346

Qy 341 GRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDE 400
Db 347 GTFKHQNNAQSMWMAFNREVPKPRPGCSPDST-----KLPENTVSFILHHPLLHR 398

Qy 401 AVPSIFNRPWFLRTMVRYLTKIAV---DTAAGPYQNHTVVFLGSEKGIILKFLARIGNS 457
Db 399 PIPSV-AAPLLVEGADRDLTQITVLPRVRAVGGH-NYDILFIGTSDGKVLKVVEVDGNA 456

Qy 458 GFLND-SLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCE 516
Db 457 TVIQSATVFQRGPPIVN-----LLTTKESVVIVSADEIASLPVHNCA 498

Qy 517 RHGKCKKTCIASRDPCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN 576
Db 499 QQTSCSK-CVQLQDPHCAWDSSIARCVHGGSWTGDQFIQNMVFGQSE---QCPEGIIV-- 552

Qy 577 GHSSSLPSTTSDSTAQEYESRGGMWDWKHLLDSPDSTDPLGAVSSHNHQDKKGIRE 636
Db 553 -----REVFDDNESEAQPEAVS-----RS 571

Qy 637 SYLKGDQLPVTLLAIAVILAFLVMGAVFSGITVYCVCDHRRKDVAVQRKEKELTHS-- 694
Db 572 GYPKEHSTITVVLVAAVASLISLIIGA-FIGIRV----NRWAATSEPHRSASSTSGSDY 625

Qy 695 -----RRGSMSSVTKLSQLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKA 745
| |::: ||: | : | : | : | : | : |

Db 626 DSFGRARLTRHDSLTTATKVDHGF-----VPQSKQSVDATSLVMSINA 668
Qy 746 DQHHLDLTALPTPESTPT 763
| : :: : :||:
Db 669 THHPMSMSQHGSGINTPS 686

RESULT 12

C49423

semaphorin II precursor - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999
C;Accession: C49423
R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.
Cell 75, 1389-1399, 1993
A;Title: The Semaphorin genes encode a family of transmembrane and secreted
growth cone guidance molecules.
A;Reference number: A49423; MUID:94094332; PMID:8269517
A;Accession: C49423
A;Status: preliminary; nucleic acid sequence not shown; not compared with
conceptual translation
A;Molecule type: mRNA
A;Residues: 1-724 <KOL>
A;Cross-references: GB:L26083
C;Genetics:
A;Gene: sema II
A;Cross-references: FlyBase:FBgn0011260
C;Superfamily: semaphorin

Query Match 14.3%; Score 779.5; DB 2; Length 724;
Best Local Similarity 33.5%; Pred. No. 4.1e-44;
Matches 193; Conservative 99; Mismatches 199; Indels 85; Gaps 22;

Qy 33 NYTKQYPVFVGHKPGRTTQRHRLD-----IQMIMIMN--GTLYIAARDHIYTV 79
| : : | |: | | :| | || |||: | | :: |

Db 32 NFYYERPCCTGNDQGNNNYKGKHGADHVREFNCGKLYYRTFHMNEDRDTLYVGAMDRVFRV 91

Qy 80 DIDTSHTEEIYCSK-KLTWKSQRADVDTCRMKGKHK-DECHNFIVKLLKKND-DALFVCG 136
:: : |:: : : : || :| || : : | | :: | : | |:||

Db 92 NLQNISSSN--CNRDAINLEPTRDDVVSCVSKGKSQIFDCKNHVRVIQSMDQGDRLYVCG 149

Qy 137 TNAFPNSCRNY-----KMDTLEPGDEFSGMARCPTYDAKHANVALFADG---- 180
||| || :| : : | : | | :||| : |:: : | |:||

Db 150 TNAHNP--KDYVIYANILHLPSEYVIGVG---LGIAKCPYDPLDNSTAIYVENGNPGL 204

Qy 181 -KLYSATVTDFLAIDAVIYRS-----LGESPTLRTVKHDSKWLKEPYFVQAVDYGDY 231
||| | :| | | :| : | | :||| : | || : | |:|

Db 205 PGLYSGTNAEFTKADTVIFRTDLYNTSAKRLEYKFKRTLKYDKWLDKPNFVGSDIGEY 264

Qy 232 IYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHF 291
:||||| | ||| | | | :| :||| | :|| : | | :||| | :| |

Db 265 VYFFFRETAVEYINCGKAVYSRIARVCKKDVGGS-KNLLAHNWATYLKARLNCSISGEFPF 323

Qy 292 YFNILQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDS 351
||| :| :| : | | | :| | : | | :||| | :|

Db 324 YFNEIQSVYQLPSDKSR--FFATFTTSTNGLIGSAVCSFHINEIQAAGNGKFKEQSSNS 381

Qy	352	TWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRP-W	410
		: : : : : :	
Db	382	AWLPVLNSRVPEPRPGTCVNNTS-----NLPDTVLNFIRSHPLMDKAVNHEHNNPVY	433
Qy	411	FLRTMVRYRLT--KIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLFLLEE	468
		: : : : : : : : :	
Db	434	YKRDLVFTKLVVDKIRIDIL--NQEYIVYYVGTNLGRUYKIVQYYRNGESLSKLLDIFE	490
Qy	469	MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC-ERHGKCKKTCIA	527
		:: :: : : : : :: : : :	
Db	491	VA-----PNEAIQVMEISQTRKSLYIGTDHRIKQTDLAMCNRRYDNCFR-CV-	536
Qy	528	SRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTD	563
		:	
Db	537	-RDPYCGWDKEANTCRPY---ELDLLQDVANETSD	567

RESULT 13

G02173

semaphorin III family homolog - human

C; Species: *Homo sapiens* (man)

C;Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text change 24-Sep-1999

C;Accession: G02173

R; Naylor, S.

submitted to the EMBL Data Library, October 1995

A; Reference number: G09275

A;Accession: G02173

A; Status: preliminary;

A; Molecule type: mRNA

A; Residues: 1-753 <NAY>

A; Cross-references: EMBL:U

Query Match 14.1%; Score 768; DB 2; Length 753;
Best Local Similarity 31.6%; Pred. No. 2.5e-43;
Matches 191; Conservative 109; Mismatches 207; Indels 98; Gaps 22.

Qy 6 LLLYFTLLHFGAGAGFPEDSEPIISIHSNYTKQYPVFGHKPGRNTTQRHRLDIQMI---- 61
 ||| : : || | | || | | | | | : :
 Db 6 LLLWASLIITGAWPSPFTOD----- HIR-----ATPPVPLSEKEKATC 43

```

Qy      103 DVDTCRMKGKH-KDECHNFIKVLLKKNDALFVCGTNAFPNSC-----RNYKMDTL 152
       :: | : || || ||::: | .:||| | :|| | :| : |
Db      100 RIEECVLSGKDVGFCGNFVBLIOPWNPTHLYVGCTGAXNPMTYVNPGRBQDVKY 152

```

QY 153 EPFGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFAIDAVIYRSLGESPTLRTVKH 212
|| | || : || | : : : || : || | : || : || : || :
Pb 159 EPERLE-SGKGKCPYDRKLDTASALINEELYACWVLFEMCTDANLEPTLGHOTNMPTDQH 217

Qy 213 DSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQ 266
Pb :|:|| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
218 NSPWLNDSSEHAEELIPESSAENDDKLVVEEPEERPSGE LPPGSGAATLLEEDDLSLWVQVQ

RESULT 14

I48748
semaphorin E - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I48748
R;Puschel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.
A;Reference number: I48744; MUID:95267431; PMID:7748561
A;Accession: I48748
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-751 <RES>
A;Cross-references: EMBL:X85994; NID:g854331; PIDN:CAA59986.1; PID:g854332
C;Genetics:
A;Gene: semE
C;Superfamily: semaphorin

Query Match 13.5%; Score 737; DB 2; Length 751;
Best Local Similarity 31.3%; Pred. No. 3e-41;
Matches 187; Conservative 103; Mismatches 234; Indels 74; Gaps 18;

Qy	24	SEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMI--MNGTLYIAARDHIYTVDI	81
		:: : ::::: : : :: ::::	
Db	42	SEYFSLSH-----QQLDYRILLMDEDQDRIYVGSKDHILSLNI	79
Qy	82	DTSHTEEIYCSKKLTWKSQRADVTCRMKGKHDE-CHNFIKVLLKKNDALFVCGTNAF	140
		: : : : : :: : :: :	
Db	80	NNISQEPL---SVFWPASTIKVEECKMAGKDPTHGCNFGVRVIQTFRTHLYVCGSGAF	135

RESULT 15

S66498

M-sema F protein precursor - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text change 24-Nov-1998

C;Accession: S66498

R; Inagaki, S.; Furuyama, T.; Iwahashi, Y.
FEBS Lett. 370 269-272 1995

A:Title: Identification of a member of mouse somatotropin family

A: Reference number: S66498; MUID: 95385800; PMID: 7655621

A, Reference number:
A:Accession: S66408

A:Accession: 366498
A:Status: preliminary

A:status: preliminary
A:Molecule type: mRNA

A, molecule type: mRNA

A:Residues: 1-834 <IN>
A:Cross-references: EMBL: S70463 - NID: 1112500

C; superfamily: semaphorin
E1-21/P; isoform: 1

F;1-21/Domain: signal sequence #status predicted <SIG>
E-22.024/Polymerase II promoter

F;22-834/Product: M-sema F protein #status predicted <MAT>

Query Match 12.7%; Score 692; DB 2; Length 834;
Best Local Similarity 26.0%; Pred. No. 3.7e-38;
Matches 232; Conservative 131; Mismatches 326; Indels 204; Gaps 34;

QY 65 NGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSRQADVDTCRMKGK-HKDECHNFIKV 123

Db	62	SGLLYVGAREALFAFSV----EALELQGAISSWAPAEKKIECTQKGKSNQTECFNFIRF	116
Qy	124	LLKKNDALFVCGTNNAFPSCRNYKMDTLEPGDEF-SGMARCPYDAKHANVALFADGKL	182
Db	117	LQPYNSSHLYVCPTYAFQPKCTYINMLTFTLDRAEFEDGKGKCPYDPAKGHTGLVDGEL	176
Qy	183	YSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWKEPYFVQA-----VDYGDYI	232
Db	177	YSATLNFLGTEPVILRYMGTHSIKT-EYLAFWLNEPHFVGSAFVPESVGSFTGDDDKI	235
Qy	233	YFFFREIAVEYNTMGKVVFPRTVAQVCKNDMGGSQRVLEKQWTSFLKARLNCVPGDSHFY	292
Db	236	YFFFSERAVEYDCYSEQVVARVARVCKGDMGGA-RTLQKKWTTFLKARLVC SAP-DWKVY	293
Qy	293	FNILQAVTDVIRINGRDVV-LATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDS	351
Db	294	FNQLKAVHTLRGASWHNTFFGVFQARWGMDLSAVCEYQLEQIQQQVFEQGPYKEYSEQAQ	353
Qy	352	TWTTPVDPERVPKPRPGCCAGSSSLER-YATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW	410
Db	354	KWARYTDP-VPSPRPGSCINNWHRDNGYTSSLELPDNTLNFIKKHPLMEDQVKPRLGRPL	412
Qy	411	FLRTMVRYRLTKIAVDTAAG-PYQNHTVVFLGSEKGIILKFLARIGNSGFLNDL-----	464
Db	413	LVKKNTNF--THVADRVPGLDGATYTVLFIGTGDGWLLKAV-----SLGPWIH	459
Qy	465	FLEEMSVNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKKT	524
Db	460	MVEELQVFDQE-----VESLVLSQSJKVLFAGRSRSQLVQLSLADCTKYRFC-VD	508
Qy	525	CIASRDPYCGWIKEGGAC-----SHLS--PNSRLTFEQDIER-----	559
Db	509	CVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYGIKKVRSIPKNITV	568
Qy	560	-GNTDGLGDCHNSFVALNGH--SSSLLPSTTSDSTAQEYESRGMLDWKHLLDSPDS	615
Db	569	VSGTDLVLPCHLSSNLAAHWTFGSQDLPAEQPGSFLYDTGLQALVVM-----	616
Qy	616	TDPLGAVSSH-----HQDKKG--VIRESYLKG-----HDQLVPVTLLAIAVILAFV	660
Db	617	---AAQSRHSGPYRCYSEEQTRLAASESYLVAVVAGSSVTLEARAPLENGLVWLAVVA	672
Qy	661	MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPE	720
Db	673	LGAVCL-VLLLLVSLRRLR-----LREELE-----KGAKAS-----ER	704
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREW--	777
Db	705	TLVYPL-----ELPKEPASPPF--RPGPETDEKLWDPV	735
Qy	778	-----ERNQNLLINACTKDMPPMGSPVIPTDPLRASPSPHIPSVVVLPIQQGYQHEYVDQ	832
Db	736	GYYYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLPS--PTRLHLGGGRNSNANGYVR-	792
Qy	833	PKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQRE	885

Db 793 -----LQLGGEDRGGS-----GHPLPELADELRRKLQQRQ 822

Search completed: March 24, 2004, 13:17:10
Job time : 33.8439 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 13:14:29 ; Search time 74.7731 Seconds
(without alignments)
3567.110 Million cell updates/sec

Title: US-09-856-681A-2

Perfect score: 5450

Sequence: 1 MRSEALLLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

1	5450	100.0	1030	12	US-10-016-248-63	Sequence 63, Appl
2	5431.5	99.7	1047	12	US-10-403-676-48	Sequence 48, Appl
3	5431.5	99.7	1047	15	US-10-449-548-48	Sequence 48, Appl
4	5422.5	99.5	1047	10	US-09-957-187-85	Sequence 85, Appl
5	5422.5	99.5	1047	12	US-10-403-676-14	Sequence 14, Appl
6	5422.5	99.5	1047	15	US-10-449-548-14	Sequence 14, Appl
7	5368	98.5	1018	12	US-10-403-676-28	Sequence 28, Appl
8	5368	98.5	1018	15	US-10-449-548-28	Sequence 28, Appl
9	5349.5	98.2	1035	12	US-10-403-676-18	Sequence 18, Appl
10	5349.5	98.2	1035	15	US-10-449-548-18	Sequence 18, Appl
11	5134.5	94.2	998	12	US-10-403-676-20	Sequence 20, Appl
12	5134.5	94.2	998	15	US-10-449-548-20	Sequence 20, Appl
13	5113.5	93.8	981	12	US-10-403-676-30	Sequence 30, Appl
14	5113.5	93.8	981	15	US-10-449-548-30	Sequence 30, Appl
15	5109.5	93.8	971	12	US-10-403-676-46	Sequence 46, Appl
16	5109.5	93.8	971	15	US-10-449-548-46	Sequence 46, Appl
17	4921	90.3	939	10	US-09-957-187-4	Sequence 4, Appl
18	4921	90.3	939	12	US-10-403-676-32	Sequence 32, Appl
19	4921	90.3	939	15	US-10-449-548-32	Sequence 32, Appl
20	4590.5	84.2	884	10	US-09-957-187-6	Sequence 6, Appl
21	4346.5	79.8	888	12	US-10-016-248-64	Sequence 64, Appl
22	3373	61.9	630	10	US-09-957-187-30	Sequence 30, Appl
23	3368	61.8	861	12	US-10-403-676-52	Sequence 52, Appl
24	3368	61.8	861	15	US-10-449-548-52	Sequence 52, Appl
25	3367.5	61.8	636	12	US-10-403-676-36	Sequence 36, Appl
26	3367.5	61.8	636	15	US-10-449-548-36	Sequence 36, Appl
27	3363	61.7	666	12	US-10-403-676-56	Sequence 56, Appl
28	3363	61.7	666	15	US-10-449-548-56	Sequence 56, Appl
29	3362	61.7	626	10	US-09-957-187-83	Sequence 83, Appl
30	3362	61.7	626	12	US-10-403-676-34	Sequence 34, Appl
31	3362	61.7	626	15	US-10-449-548-34	Sequence 34, Appl
32	3351.5	61.5	649	12	US-10-403-676-50	Sequence 50, Appl
33	3351.5	61.5	649	15	US-10-449-548-50	Sequence 50, Appl
34	3349.5	61.5	878	12	US-10-403-676-54	Sequence 54, Appl
35	3349.5	61.5	878	15	US-10-449-548-54	Sequence 54, Appl
36	3285.5	60.3	640	12	US-10-403-676-16	Sequence 16, Appl
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38	2627	48.2	497	12	US-10-403-676-24	Sequence 24, Appl
39	2627	48.2	497	15	US-10-449-548-24	Sequence 24, Appl
40	2545	46.7	479	12	US-10-403-676-26	Sequence 26, Appl
41	2545	46.7	479	15	US-10-449-548-26	Sequence 26, Appl
42	2349.5	43.1	1088	12	US-10-016-248-20	Sequence 20, Appl
43	2335	42.8	1035	12	US-10-016-248-12	Sequence 12, Appl
44	2330	42.8	442	12	US-10-403-676-22	Sequence 22, Appl
45	2330	42.8	442	15	US-10-449-548-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
 US-10-016-248-63
 ; Sequence 63, Application US/10016248
 ; Publication No. US20040033491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsobrook et al.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 1030
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-016-248-63

Query Match 100.0%; Score 5450; DB 12; Length 1030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 60
Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120
Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120

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Db 121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDFSGMARCYDAKHANVALFADG 180

Qy 181 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
Db 181 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy 241 VEYNTMGKVVFPRVAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
Db 241 VEYNTMGKVVFPRVAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
Db 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
Db 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD	480
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Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGCKKTCIASRDPYCGWIKEGG	540
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Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESR	600
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Qy	781	QNLINACTKDMPPMGSPVIPTDPLRASPShIPSvvlpITQQGYQHEYVDQPKMSEVAQ	840
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Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDLSPPKVPQREASLGPPGASLSQTGL	900
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Qy	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSSLRSRNQSFGRGDNPP	960
Db	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSSLRSRNQSFGRGDNPP	960
Qy	961	PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPLKPDVPPKPSFAPLS	1020
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Qy	1021	TSMKPNDACT 1030	
Db	1021	TSMKPNDACT 1030	

RESULT 2

US-10-403-676-48

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; Sequence 48, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
```

; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 48
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-48

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Best Local Similarity 98.4%; Pred. No. 0;
Matches 1030; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

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Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPISHGNYTKQYPFVGHKPGRNTTQRHRLDIQM 60

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Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120

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Db 121 IKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPTYDAKHANVALFADG 180

QY 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240
Db 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240

QY 241 VEYNTMGKVVFPRVAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDHFYFNILQAVT 300
Db 241 VEYNTMGKVVFPRVAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDHFYFNILQAVT 300

QY 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
Db 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

QY 361 VPKPGRPCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
Db 361 VPKPGRPCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

QY 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFEEMSVYNSEKCSYD 480
Db 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFEEMSVYNSEKCSYD 480

QY 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKKTCIASRDPYCGWIKEGG 540
Db 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKKTCIASRDPYCGWIKEGG 540

QY 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSLL 583
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Qy 584 PSTTTSSTAQEYESRGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLGHD 643
Db 601 PSTTTSSTAQEYESRGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLGHD 660

Qy 644 QLVPVTLLAIHAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT 703
Db 661 QLVPVTLLAIHAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT 720

Qy 704 KLSGLFGDTQSKEPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLTLALPTPESTPT 763
Db 721 KLSGLFGDTQSKEPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLTLALPTPESTPT 780

Qy 764 LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPIQQ 823

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Db 781 LQQKRKPSRGSREWERNQNLINACTKDMP PMGSPVIPTDLPLRASP SHIPS VVVL PITQQ 840
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QY 824 GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLS SKSPN HGVNLVENLDSLPPKVPQ 883
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QY 884 REASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSL TRSHQATTLKRNNTN SNN 943
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Db 1021 PSLKPDVPPKPSFAPLSTS MKPND ACT 1047

RESULT 3

US-10-449-548-48

; Sequence 48, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: US/10/449,548

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 60/234,082

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: 60/233,798

; PRIOR FILING DATE: 2000-09-19

; PRIOR APPLICATION NUMBER: 60/174,485

; PRIOR FILING DATE: 2000-01-04

; PRIOR APPLICATION NUMBER: 10/403,676

; PRIOR FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/384,798

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: 60/402,407

; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 48
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-48

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Query Match          99.7%;  Score 5431.5;  DB 15;  Length 1047;
Best Local Similarity 98.4%;  Pred. No. 0;
Matches 1030;  Conservative 0;  Mismatches 0;  Indels 17;  Gaps 1;

Qy      1 MRSEALLLYFTLLLHFAGAGFPEDSEPIISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 60
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Db      1 MRSEALLLYFTLLLHFAGAGFPEDSEPIISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 60

Qy      61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGKHDECHNF 120
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGKHDECHNF 120

Qy      121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCPTYDAKHANVALFADG 180
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCPTYDAKHANVALFADG 180

Qy      181 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy      241 VEYNTMGKVVFPRAVQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDHFYFNILQAVT 300
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Db      241 VEYNTMGKVVFPRAVQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDHFYFNILQAVT 300

Qy      301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy      361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
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Db      361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy      421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNSEKCSYD 480
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Qy      541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSLL 583
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Db      541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSYNTVYGHSSLL 600

Qy      584 PSTTTSSTAQEYESRGGMLDWKHLLSPDSTDPLGAVSSHNHQDKKGVIRESYLGHD 643
        ||||||| | | | | | | | | | | | | | | | | | | | | | | |

```

Db 601 PSTTTSSTAQEYESRGGMLDWKHLLSPDSTDPLGAVSSHQDKKGVIRESYLGHD 660
 QY 644 QLVPVTLLAIAVILAFVMGAVFSGITVYCVCDDHRRKDVAVVQRKEKELTHSRRGSMSSVT 703
 |||||||
 Db 661 QLVPVTLLAIAVILAFVMGAVFSGITVYCVCDDHRRKDVAVVQRKEKELTHSRRGSMSSVT 720
 QY 704 KLSGLFGDTQSKEPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLTLALPTPESTPT 763
 |||||||
 Db 721 KLSGLFGDTQSKEPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLTLALPTPESTPT 780
 QY 764 LQQKRKPSSRGSREWERNQNLIINACTKDMPPMGSPVIPTDLPLRASPShIPSVVVLPIQQ 823
 |||||||
 Db 781 LQQKRKPSSRGSREWERNQNLIINACTKDMPPMGSPVIPTDLPLRASPShIPSVVVLPIQQ 840
 QY 824 GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHNVLVENLDSLPPKVPQ 883
 |||||||
 Db 841 GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHNVLVENLDSLPPKVPQ 900
 QY 884 REASLGPPGASLSQTGLSKRLEMHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSN 943
 |||||||
 Db 901 REASLGPPGASLSQTGLSKRLEMHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSN 960
 QY 944 SSHLSRNQSFGRGDNPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLRSGLKRT 1003
 |||||||
 Db 961 SSHLSRNQSFGRGDNPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLRSGLKRT 1020
 QY 1004 PSLKPDVPPKPSFAPLSTS MKPND ACT 1030
 |||||||
 Db 1021 PSLKPDVPPKPSFAPLSTS MKPND ACT 1047

RESULT 4

US-09-957-187-85

```

; Sequence 85, Application US/09957187
; Publication No. US20030054514A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: LaRochelle, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 1047
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-957-187-85

Query Match 99.5%; Score 5422.5; DB 10; Length 1047;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1029; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPI SISHCNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGKHDECHNF 120
Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGKHDECHNF 120

Qy 121 IKVLLKKNDDALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGM ARCPYDAKHANVALFADG 180
Db 121 IKVLLKKNDDALFVCGTNAFNPS CRNYKMDTLEPFGDEFSGM ARCPYDAKHANVALFADG 180

Qy 181 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240
Db 181 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240

Qy 241 VEYNTMGKVVFP RVAQVCKNDMGG SQRVLEKQWTSFLKARLNCSV PGDSH FYFNILQAVT 300
Db 241 VEYNTMGKVVFP RVAQVCKNDMGG SQRVLEKQWTSFLKARLNCSV PGDSH FYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGS AVCAYDMLDIASVFTGRFKEQKSPD STWTPVPDER 360
Db 301 DVIRINGRDVVLATFSTPYNSIPGS AVCAYDMLDIASVFTGRFKEQKSPD STWTPVPDER 360

Qy 361 VP KPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEA VPSIFNRPWFLRTMVRYRL 420
Db 361 VP KPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEA VPSIFNRPWFLRTMVRYRL 420

Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 480
Db 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYD 480

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHGKCKTCIASRDPYCGWIKEGG 540
Db 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHGKCKTCIASRDPYCGWIKEGG 540

Qy 541 AC SHLSPNSRLTFEQ DIERGNTDGLGDCHNSFVALN-----GHSSSL 583
Db 541 AC SHLSPNSRLTFEQ DIERGNTDGLGDCHNSFVALNDISTPLPDNEMS YNTVYGHSSSL 600

Qy 584 P STTTSDSTAQE YESRGGM LDWKHLLDSPDSTDPLGA VSSH NHQDKKGVIRESY LGHD 643
Db 601 P STTTSDSTAQE YESRGGM LDWKHLLDSPDSTDPLGA VSSH NHQDKKGVIRESY LGHD 660

Qy 644 Q LVPVTLLAI AIVI LAFVMGAVFSGITVYCVCDHRRKDVA VQRKEKELTHSRRGSMSSVT 703
Db 661 Q LVPVTLLAI AIVI LAFVMGAVFSGITVYCVCDHRRKDVA VQRKEKELTHSRRGSMSSVT 720

Qy 704 KLSGLFGDTQS KDPKPEA ILTPLMHNGKLATPGNTAKMLI KADQHLDLTALPTPESTPT 763
Db 721 KLSGLFGDTQS KDPKPEA ILTPLMHNGKLATPGNTAKMLI KADQHLDLTALPTPESTPT 780

Db	721 KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPT	780
QY	764 LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPShIPSVVVLPIQQ	823
Db	781 LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPShIPSVVVLPIQQ	840
QY	824 GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	883
Db	841 GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ	900
QY	884 REASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSN	943
Db	901 REASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSN	960
QY	944 SSHLSRNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003
Db	961 SSHLSRNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1020
QY	1004 PSLKPDVPPKPSFAPLSTSMKPNDACT	1030
Db	1021 PSLKPDVPPKPSFAPLSTSMKPNDACT	1047

RESULT 5

US-10-403-676-14

; Sequence 14, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 14
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-14

Query Match 99.5%; Score 5422.5; DB 12; Length 1047;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1029; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

Qy	1 MRSEALLLYFTLLHFAGAGFPEDSEPISHGNYTKQYPFVGHKPGRNTTQRHRLDIQM 60
Db	1 MRSEALLLYFTLLHFAGAGFPEDSEPISHCNYTKQYPFVGHKPGRNTTQRHRLDIQM 60
Qy	61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHDECHNF 120
Db	61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHDECHNF 120
Qy	121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPFGDESGMARCPYDAKHANVALFADG 180
Db	121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPFGDESGMARCPYDAKHANVALFADG 180
Qy	181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
Db	181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
Qy	241 VEYNTMGKVVFPRVAQVCKNDMGGSQLKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
Db	241 VEYNTMGKVVFPRVAQVCKNDMGGSQLKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy	301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Qy	361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Qy	421 TKIAVDTAAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDLSLFLEEMSVNSEKCSYD	480
Db	421 TKIAVDTAAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDLSLFLEEMSVNSEKCSYD	480
Qy	481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKKTCIASRDPYCGWIKEGG	540
Db	481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKKTCIASRDPYCGWIKEGG	540
Qy	541 ACSHLSPNSRLTFeQDIERGNTDGLGDCHNSFVALN-----GHSSLL	583
Db	541 ACSHLSPNSRLTFeQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSNTVYGHSSLL	600
Qy	584 PSTTTSDSTAQEYESRGMLDWKHLLDSDPSTDPLGAVSSHNDQDKGVIRESYLKHD	643
Db	601 PSTTTSDSTAQEYESRGMLDWKHLLDSDPSTDPLGAVSSHNDQDKGVIRESYLKHD	660
Qy	644 QLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT	703
Db	661 QLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT	720
Qy	704 KLSGLFGDTQS KDPKPEAILTPI MHNGKLATPGNTAKMLI KADQH HLDLTALPTPESTPT	763
Db	721 KLSGLFGDTQS KDPKPEAILTPI MHNGKLATPGNTAKMLI KADQH HLDLTALPTPESTPT	780
Qy	764 LQQKRKP SRGSREWERNQN LINACTKDMPPM GSPVIPTDLPLRASP SHIPS VVVL PITQQ	823
Db	781 LQQKRKP SRGSREWERNQN LINACTKDMPPM GSPVIPTDLPLRASP SHIPS VVVL PITQQ	840
Qy	824 GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEH LSSKSPN HGVNLVENLDSL PPKV P Q	883
Db	841 GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEH LSSKSPN HGVNLVENLDSL PPKV P Q	900
Qy	884 REASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSN	943
Db	901 REASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSN	960
Qy	944 SSHLSRNQS FGRGDNP P PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1003
Db	961 SSHLSRNQS FGRGDNP P PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT	1020
Qy	1004 PSLKPDVPPKPSFAPLSTS MKPND ACT	1030
Db	1021 PSLKPDVPPKPSFAPLSTS MKPND ACT	1047

RESULT 6

US-10-449-548-14

; Sequence 14, Application US/10449548

; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 14
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-14

Query Match 99.5%; Score 5422.5; DB 15; Length 1047;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1029; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHCNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGHKDECHNF 120
Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGHKDECHNF 120

Qy 121 IKVLLKKNDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCYDAKHANVALFADG 180
Db 121 IKVLLKKNDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCYDAKHANVALFADG 180

Qy 181 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
Db 181 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy 241 VEYNTMGKVVFPRAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
Db 241 VEYNTMGKVVFPRAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSACAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
Db 301 DVIRINGRDVVLATFSTPYNSIPGSACAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
Db 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

Qy 421 TKIAVDTAAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLFEEMSVYNSEKCSYD 480
Db 421 TKIAVDTAAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLFEEMSVYNSEKCSYD 480

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 540
Db 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 540

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GHSSSL 583
Db 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSNTVYGHSSSL 600

Qy 584 PSTTTSDSTAQEYESRGMLDWKHLLSPDSTDPLGAVSSHNDQDKKGVIRESYLGHD 643
Db 601 PSTTTSDSTAQEYESRGMLDWKHLLSPDSTDPLGAVSSHNDQDKKGVIRESYLGHD 660

Qy 644 QLVPVTLLAIAVILAFLVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT 703
Db 661 QLVPVTLLAIAVILAFLVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVT 720

Qy 704 KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHLDLTALPTPESTPT 763
Db 721 KLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHLDLTALPTPESTPT 780

Qy 764 LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPISHIPSVVVLPIQQ 823
Db 781 LQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPISHIPSVVVLPIQQ 840

Qy 824 GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ 883
Db 841 GYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQ 900

Qy 884 REASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSN 943
Db 901 REASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSN 960

Qy 944 SSHLSRNQSFRGDNPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT 1003

Db 961 |||||||SSHLSRNQSFGRGDNPPPAPQRVDSIQVHSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT 1020
QY 1004 PSLKPDVPPKPSFAPLSTSMKPNDACT 1030
|||
Db 1021 PSLKPDVPPKPSFAPLSTSMKPNDACT 1047

RESULT 7

US-10-403-676-28

; Sequence 28, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE

; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 28
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-28

Query Match 98.5%; Score 5368; DB 12; Length 1018;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1013; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	17	GAGFPEDSEPISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	76
Db	2	GSGFPEDSEPISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	61
Qy	77	YTVIDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGHKDECHNFIKVLLKKNDALFVCG	136
Db	62	YTVIDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGHKDECHNFIKVLLKKNDALFVCG	121
Qy	137	TNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV	196
Db	122	TNAFNPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYSATVTDFLAIDAV	181
Qy	197	IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVEYNTMGKVVFPRVAQ	256
Db	182	IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVEYNTMGKVVFPRVAQ	241
Qy	257	VCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDHFYFNILQAVTDVIRINGRDVVLATFS	316
Db	242	VCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDHFYFNILQAVTDVIRINGRDVVLATFS	301
Qy	317	TPYNSIPGSACVAYDMEDIAVFTGRFKEQKSPDSTWPVDERVPKPRPGCCAGSSSLE	376
Db	302	TPYNSIPGSACVAYDMEDIAVFTGRFKEQKSPDSTWPVDERVPKPRPGCCAGSSSLE	361
Qy	377	RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT	436
Db	362	RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT	421
Qy	437	VVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	496
Db	422	VVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	481
Qy	497	SSLVAFSTCVIKVPLGRCERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLTSEQD	556

Db	482	SSLYVAFSTCVIKVPLGRCERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLT FEQD	541
Qy	557	IERGNTDGLGDCHNSFVALNGHSSLLPSTTS STAQE GYESRGGM DWKHLLD SPDST	616
Db	542	IERGNTDGLGDCHNSFVALNGHSSLLPSTTS STAQE GYESRGGM DWKHLLD SPDST	601
Qy	617	DPLGAVSSH NHQDKKG VIRESYLKGHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDH	676
Db	602	DPLGAVSSH NHQDKKG VIRESYLKGHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDH	661
Qy	677	RRKDVAVVQRKEKELTHSRRGS MSVTKLSGLFGDTQS KDPKPEAILT PLMHNG KLATPG	736
Db	662	RRKDVAVVQRKEKELTHSRRGS MSVTKLSGLFGDTQS KDPKPEAILT PLMHNG KLATPG	721
Qy	737	NTAKMLIKADQHHLDLTALPTPESTPTLQQKRKP SRG SREWERNQN LINACT KDMPPMGS	796
Db	722	NTAKMLIKADQHHLDLTALPTPESTPTLQQKRKP SRG SREWERNQN LINACT KDMPPMGS	781
Qy	797	PVIPTDLPLRASP SHIPSVVLPITQQGYQHEYVDQPKMSEVAQM ALEDQAATLEYKTIK	856
Db	782	PVIPTDLPLRASP SHIPSVVLPITQQGYQHEYVDQPKMSEVAQM ALEDQAATLEYKTIK	841
Qy	857	EHLSSKSPN HGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEM HSSSYGVDY	916
Db	842	EHLSSKSPN HGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEM HSSSYGVDY	901
Qy	917	KRSYPTNSL TRSHQATT LKRNNNTSS SSHLSRNQSFGRGDNPPPAPQRVDSIQVHSSQP	976
Db	902	KRSYPTNSL TRSHQATT LKRNNNTSS SSHLSRNQSFGRGDNPPPAPQRVDSIQVHSSQP	961
Qy	977	SGQAVTVSRQPSLNAYNSL TRSGLKRTPSLKPDVPPKPSFAPLSTMKPND ACT	1030
Db	962	SGQAVTVSRQPSLNAYNSL TRSGLKRTPSLKPDVPPKPSFAPLSTMKPND ACT	1015

RESULT 8

US-10-449-548-28

```

; Sequence 28, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03

```

; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 28
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-449-548-28

Query Match 98.5%; Score 5368; DB 15; Length 1018;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1013; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 17 GAGFPEDSEPISHGNYTKQYPVFVGHKPGRTTQRHRLDIQMIMIMNGTLYIAARDHI 76
| :|||||||||||||||||||||||||||||||||||||||||||||||||
Db 2 GSGFPEDSEPISHGNYTKQYPVFVGHKPGRTTQRHRLDIQMIMIMNGTLYIAARDHI 61

Qy 77 YTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHDECHNFIKVLLKKNDDALFVCG 136
|||||||||||||||||||||||||||||||||||||||||||||
Db 62 YTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHDECHNFIKVLLKKNDDALFVCG 121

Qy 137 TNAFNPSCKNYKMDTLEPGDEFSGMARCPTYDAKHANVALFADGKLYSATVTDI 196
|||||||||||||||||||||||||||||||||||||||||
Db 122 TNAFNPSCKNYKMDTLEPGDEFSGMARCPTYDAKHANVALFADGKLYSATVTDI 181

Qy 197 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ 256
|||||||||||||||||||||||||||||||||||||||||
Db 182 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVEYNTMGKVVFPRVAQ 241

Qy 257 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 316
|||||||||||||||||||||||||||||||||||||||||
Db 242 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 301

Qy 317 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSLE 376
|||||||||||||||||||||||||||||||||||||
Db 302 TPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSLE 361

Qy 377 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYLTKIAVDTAAGPYQNHT 436
|||||||||||||||||||||||||||||||||||||
Db 362 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYLTKIAVDTAAGPYQNHT 421

Qy	437	VVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	496
Db	422	VVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	481
Qy	497	SSLYVAFSTCVIKVPLGRcerHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLTFeQD	556
Db	482	SSLYVAFSTCVIKVPLGRcerHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLTFeQD	541
Qy	557	IERGNTDGLGDCHNSFVALNGHSSLLPSTTSdstaqegyesrggmldwkhllldspdst	616
Db	542	IERGNTDGLGDCHNSFVALNGHSSLLPSTTSdstaqegyesrggmldwkhllldspdst	601
Qy	617	DPLGAVSSHNNHQDKKGVIRESYLGKHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDH	676
Db	602	DPLGAVSSHNNHQDKKGVIRESYLGKHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDH	661
Qy	677	RRKDVAVVQRKEKELTHSRRGSMSSVTLSGLFGDTQS KDPKPEAILTPLMHNGKLATPG	736
Db	662	RRKDVAVVQRKEKELTHSRRGSMSSVTLSGLFGDTQS KDPKPEAILTPLMHNGKLATPG	721
Qy	737	NTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGREWERNQNLINEACTKDMPPMGS	796
Db	722	NTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGREWERNQNLINEACTKDMPPMGS	781
Qy	797	PVIPTDLPLRASPShIPSvvvlpitQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTik	856
Db	782	PVIPTDLPLRASPShIPSvvvlpitQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTik	841
Qy	857	EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDY	916
Db	842	EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDY	901
Qy	917	KRSYPTNSLRSHQATTLKRNNTNSSNSHLSRNQSFGRGDNP PAPQRVDSTIQVHSSQP	976
Db	902	KRSYPTNSLRSHQATTLKRNNTNSSNSHLSRNQSFGRGDNP PAPQRVDSTIQVHSSQP	961
Qy	977	SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKDVPVPPKPSFAPLSTMKPNDACT	1030
Db	962	SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKDVPVPPKPSFAPLSTMKPNDACT	1015

RESULT 9

US-10-403-676-18

; Sequence 18, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 18
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-403-676-18

Query Match 98.2%; Score 5349.5; DB 12; Length 1035;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1013; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

Qy	17	GAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	76
	1:		
Db	2	GSGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMNGTLYIAARDHI	61
Qy	77	YTV DIDTSHTEE IYCSKKLTWKS RQAD VDT CRMKGHK DECHNFIKVLLKKNDDALFVCG	136
Db	62	YTV DIDTSHTEE IYCSKKLTWKS RQAD VDT CRMKGHK DECHNFIKVLLKKNDDALFVCG	121
Qy	137	TNAFN PSCR NYKMDT LEPFGDEF SG MARCPY DAKHAN VAL FADG KLY SAT VTD FLAIDAV	196
Db	122	TNAFN PSCR NYKMDT LEPFGDEF SG MARCPY DAKHAN VAL FADG KLY SAT VTD FLAIDAV	181
Qy	197	IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVEYNTMGKVVFPRAQ	256
Db	182	IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVEYNTMGKVVFPRAQ	241
Qy	257	VCKNDMGG SQRV LEKQW TSFL KARLN CSVP GD SHFY FN ILQAV T DVIR IN GRDV VLAT FS	316
Db	242	VCKNDMGG SQRV LEKQW TSFL KARLN CSVP GD SHFY FN ILQAV T DVIR IN GRDV VLAT FS	301
Qy	317	TPYNSIPGS AVCAYDMLDIASVFTGRFKEQKSPDSTWTPV PDER VP KPRPG CAGSSLE	376
Db	302	TPYNSIPGS AVCAYDMLDIASVFTGRFKEQKSPDSTWTPV PDER VP KPRPG CAGSSLE	361
Qy	377	RYATSNEFP DDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT	436
Db	362	RYATSNEFP DDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT	421
Qy	437	VVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	496
Db	422	VVFLGSEKGIILKFLARIGNSGFLNDSL FLEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS	481
Qy	497	SSLYVA FSTCVIKVPLGR CERHGKCKTCIASRD PYCGWIKEGGACSHLSPNSRLT FEQD	556
Db	482	SSLYVA FSTCVIKVPLGR CERHGKCKTCIASRD PYCGWIKEGGACSHLSPNSRLT FEQD	541
Qy	557	I ERGNTDGLGDCHNSFVALN-----GHSSSLPSTTS DSTA QEGYES	599
Db	542	I ERGNTDGLGDCHNSFVALNDISTPLPDNEMS YNTVY GHSSSLPSTTS DSTA QEGYES	601
Qy	600	RGGMLDWKHL LDSPDSTDPLGAVSSH NHQDKKGVI RESYLKGHDQ LVPVTLLAIVI LAF	659
Db	602	RGGMLDWKHL LDSPDSTDPLGAVSSH NHQDKKGVI RESYLKGHDQ LVPVTLLAIVI LAF	661
Qy	660	VMGA VFSGITVYCVCDHRRKDVA VVQRKEKELTHSRRGSMSSVT KLSGLFGDTQS KDPKP	719
Db	662	VMGA VFSGITVYCVCDHRRKDVA VVQRKEKELTHSRRGSMSSVT KLSGLFGDTQS KDPKP	721
Qy	720	EAILTPLMHNGKLATPGNTAKMLI KADQHHL DL TALPTPE STPTLQQKRKP SRGS REWER	779
Db	722	EAILTPLMHNGKLATPGNTAKMLI KADQHHL DL TALPTPE STPTLQQKRKP SRGS REWER	781
Qy	780	NQNLINACTKDMPPMGSPVIPTDLPLRASP SHIPS VVVL PITQQGYQHEYVDQPKMSEVA	839
Db	782	NQNLINACTKDMPPMGSPVIPTDLPLRASP SHIPS VVVL PITQQGYQHEYVDQPKMSEVA	841
Qy	840	QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSL PPKV PQREASLGPPGASLSQTG	899

Db ||||||| 842 QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG 901
QY 900 LSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSHLSRNQSFGRGDNP 959
Db ||||||| 902 LSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSHLSRNQSFGRGDNP 961
QY 960 PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL 1019
Db ||||||| 962 PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDPVPPKPSFAPL 1021
QY 1020 STSMKPNDACT 1030
Db ||||||| 1022 STSMKPNDACT 1032

RESULT 10
US-10-449-548-18
; Sequence 18, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 18
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-18

Query Match 98.2%; Score 5349.5; DB 15; Length 1035;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1013; Conservative 1; Mismatches 0; Indels 17; Gaps 1;

Qy 17 GAGFPEDSEPISHGNYTKQYPVFVGHKPGRTTQRHRLDIQMIMIMNGTLYIAARDHI 76
Db 2 GSGFPEDSEPISHGNYTKQYPVFVGHKPGRTTQRHRLDIQMIMIMNGTLYIAARDHI 61

Qy 77 YTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGHKDECHNFIKVLLKKNDDALFVCG 136
Db 62 YTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGHKDECHNFIKVLLKKNDDALFVCG 121

Qy 137 TNAFNPSCKNYKMDTLEPGDEFSGMARCPTYDAKHANVALFADGKLYSATVTDFLAIDAV 196
Db 122 TNAFNPSCKNYKMDTLEPGDEFSGMARCPTYDAKHANVALFADGKLYSATVTDFLAIDAV 181

Qy 197 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGYIYFFFREIAVEYNTMGKVVFPRVAQ 256
Db 182 IYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGYIYFFFREIAVEYNTMGKVVFPRVAQ 241

Qy 257 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 316
Db 242 VCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFS 301

Qy 317 TPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSLE 376
Db 302 TPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSLE 361

Qy 377 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT 436
Db 362 RYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHT 421

Qy 437 VVFLGSEKGIILKFLARIGNSGFLNDSLFEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS 496
Db 422 VVFLGSEKGIILKFLARIGNSGFLNDSLFEEMSVYNSEKCSYDGVEDKRIMGMQLDRAS 481

Qy 497 SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFeQD 556
Db 482 SSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFeQD 541

Qy 557 IERGNTDGLGDCHNSFVALN-----GHSSSLPSTTSSTAQEYES 599
Db 542 IERGNTDGLGDCHNSFVALNDISTPLPDNEMSNTVYGHSSSLPSTTSSTAQEYES 601

Qy 600 RGGMLDWKHLLSDPDSTDPLGAVSSHQDKKGVIRESYLYKGHDQLPVTLAIAVILAF 659
Db 602 RGGMLDWKHLLSDPDSTDPLGAVSSHQDKKGVIRESYLYKGHDQLPVTLAIAVILAF 661

Qy 660 VMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKP 719
|||||||||||||||||||||||||||||||||||||||||||||||||||||

Db	662 VMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGLFGDTQSKDPKP	721
Qy	720 EAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWER	779
Db	722 EAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWER	781
Qy	780 NQNLINACTKDMPPMGSPVIPTDPLRASPShIPSvvLPITQQGYQHEYVDQPKMSEVA	839
Db	782 NQNLINACTKDMPPMGSPVIPTDPLRASPShIPSvvLPITQQGYQHEYVDQPKMSEVA	841
Qy	840 QMALEDQAATLEYKTIKEHLSSKSPNHNVLVENLDSLPPKVPQREASLGPPGASLSQTG	899
Db	842 QMALEDQAATLEYKTIKEHLSSKSPNHNVLVENLDSLPPKVPQREASLGPPGASLSQTG	901
Qy	900 LSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSSLRSRNQSFGRGDNP	959
Db	902 LSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSSLRSRNQSFGRGDNP	961
Qy	960 PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKDVPVPPKPSFAPL	1019
Db	962 PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKDVPVPPKPSFAPL	1021
Qy	1020 STSMKPNDACT 1030	
Db	1022 STSMKPNDACT 1032	

RESULT 11

US-10-403-676-20

```
; Sequence 20, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
```

; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 20
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-20

Query Match 94.2%; Score 5134.5; DB 12; Length 998;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 975; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

Qy 56 LDIQMIMIMNGTLYIAARDHIYTVIDTSHTEEYCSKKLTWKSQADVDTCRMKGKHKD 115
Db 4 LDIQMIMIMNGTLYIAARDHIYTVIDTSHTEEYCSKKLTWKSQADVDTCRMKGKHKD 63

Qy 116 ECHNFIKVLLKKNDDALFVCGTNAFPSCRNYKMDTLEPGDEFSGMARCPTYDAKHANVA 175
Db 64 ECHNFIKVLLKKNDDALFVCGTNAFPSCRNYKMDTLEPGDEFSGMARCPTYDAKHANVA 123

Qy 176 LFADGKLYSATVDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFF 235
Db 124 LFADGKLYSATVDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFF 183

Qy 236 FREIAVEYNTMGKVVFPRAQVCKNDMGGSQLVLEKQWTSFLKARLNCSVPGDSHFYFNI 295
Db 184 FREIAVEYNTMGKVVFPRAQVCKNDMGGSQLVLEKQWTSFLKARLNCSVPGDSHFYFNI 243

Qy	296	LQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTP	355
Db	244	LQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTP	303
Qy	356	VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM	415
Db	304	VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM	363
Qy	416	VRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDLSLFLEEMSVYNSE	475
Db	364	VRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDLSLFLEEMSVYNSE	423
Qy	476	KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKKTCIASRDPYCGW	535
Db	424	KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKKTCIASRDPYCGW	483
Qy	536	IKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----GH	578
Db	484	IKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMSNTVYGH	543
Qy	579	SSSLLPSTTSDSTAQEYESRGGMWDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESY	638
Db	544	SSSLLPSTTSDSTAQEYESRGGMWDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESY	603
Qy	639	LKGHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGS	698
Db	604	LKGHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGS	663
Qy	699	MSSVTKLSGLFGDTQS KDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTP	758
Db	664	MSSVTKLSGLFGDTQS KDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTP	723
Qy	759	ESTPTLQQKRKPQRSREWERNQNLINACTKDMPPMGS PVIPTDPLRASPShIPS VVVL	818
Db	724	ESTPTLQQKRKPQRSREWERNQNLINACTKDMPPMGS PVIPTDPLRASPShIPS VVVL	783
Qy	819	PITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPN HGVNLVENLDSLP	878
Db	784	PITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPN HGVNLVENLDSLP	843
Qy	879	PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRN N	938
Db	844	PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRN N	903
Qy	939	TNSSNSSHLSRNQSFGRGDNP PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS	998
Db	904	TNSSNSSHLSRNQSFGRGDNP PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS	963
Qy	999	GLKRTPSLKP DVPPKPSFAPLSTS MKPND ACT	1030
Db	964	GLKRTPSLKP DVPPKPSFAPLSTS MKPND ACT	995

RESULT 12

US-10-449-548-20

; Sequence 20, Application US/10449548

; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 20
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-449-548-20

Query Match 94.2%; Score 5134.5; DB 15; Length 998;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 975; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

Qy 56 LDIQMIMIMNGTLYIAARDHIYTVIDTSHTEEIYCSKLTWKSQADVDTCRMKGHKD 115
Db 4 LDIQMIMIMNGTLYIAARDHIYTVIDTSHTEEIYCSKLTWKSQADVDTCRMKGHKD 63

Qy 116 ECHNFIKVLLKKNDDALFVCGTNAFPSCRNYKMDTLEPGDEFSGMARCYPYDAKHANVA 175
Db 64 ECHNFIKVLLKKNDDALFVCGTNAFPSCRNYKMDTLEPGDEFSGMARCYPYDAKHANVA 123

Qy 176 LFADGKLYSATVTDLAI DAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFF 235
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 LFADGKLYSATVTDLAI DAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFF 183

Qy 236 FREIAVEYNTMGKVFP RVAQVC KNDMGG SQRV LEK QW TSFL KARLN C SVPGD SHFY FNI 295
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 FREIAVEYNTMGKVFP RVAQVC KNDMGG SQRV LEK QW TSFL KARLN C SVPGD SHFY FNI 243

Qy 296 LQAVTDVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTP 355
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 LQAVTDVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTP 303

Qy 356 VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM 415
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 VPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTM 363

Qy 416 VRYRLTKIAVDTAAGPYQNHTVVFLGSEKG IILKFLARIGNSGFLNDLFLEEMSVYNSE 475
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 VRYRLTKIAVDTAAGPYQNHTVVFLGSEKG IILKFLARIGNSGFLNDLFLEEMSVYNSE 423

Qy 476 KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGW 535
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 424 KCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CERHGKCKKTCIASRDPYCGW 483

Qy 536 IKE GGACSHLSPNSRLT FEQDIERGNTDGLGDCHNSFVALN-----GH 578
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 484 IKE GGACSHLSPNSRLT FEQDIERGNTDGLGDCHNSFVALNDISTPLPDNEMS YNTVY GH 543

Qy 579 SSLLPSTTSDSTAQE YESRG GMLDWK HLLD SP DSTDPLGA VSSHNHQDKKGVI RESY 638
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 544 SSLLPSTTSDSTAQE YESRG GMLDWK HLLD SP DSTDPLGA VSSHNHQDKKGVI RESY 603

Qy 639 LKGHDQLVPVTLLAI A VI LAFVMGA VFSGITVYCVCDHRRKDVA VQRKEKELTHSRRGS 698
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 604 LKGHDQLVPVTLLAI A VI LAFVMGA VFSGITVYCVCDHRRKDVA VQRKEKELTHSRRGS 663

Qy 699 MSSVTKL SGLFGDTQS KDPKPEA ILTPLMHN GKLATPGNTAKMLI KADQHHLDLTALPTP 758
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 664 MSSVTKL SGLFGDTQS KDPKPEA ILTPLMHN GKLATPGNTAKMLI KADQHHLDLTALPTP 723

Qy 759 ESTPTLQQKRKP SRGSREWERNQNLINACTKDMPPMGS PVIPTDLPLRASP SHIPS VVVL 818
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 724 ESTPTLQQKRKP SRGSREWERNQNLINACTKDMPPMGS PVIPTDLPLRASP SHIPS VVVL 783

Qy 819 PITQQGYQHEYVDQPKMS EVAQMALEDQAATLEYKTIEHLSSKSPNHGVNLVENLDSLP 878
||| ||| ||| ||| ||| ||| ||| |||
Db 784 PITQQGYQHEYVDQPKMS EVAQMALEDQAATLEYKTIEHLSSKSPNHGVNLVENLDSLP 843

Qy 879 PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRN N 938
||| ||| ||| ||| ||| ||| ||| |||
Db 844 PKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRN N 903

Qy 939 TNSSNSSHLSRNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS 998
||| ||| ||| ||| ||| ||| ||| |||
Db 904 TNSSNSSHLSRNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRS 963

Qy 999 GLKRTPSLKP DVPPKPSFAPLSTS MKPND ACT 1030

Db 964 GLKRTPSLKP DVPPKPSFAPLSTS MKPND ACT 995

RESULT 13

US-10-403-676-30

; Sequence 30, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE

; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 30
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-403-676-30

Query Match 93.8%; Score 5113.5; DB 12; Length 981;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 1; Indels 55; Gaps 1;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 60
Db 4 MRSEALLLYFTLLHFAGAGFPEDSEPISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 63

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120
Db 64 IMIMNGTLYIAARDHIYTVDIDTSHTEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 123

Qy 121 IKVLLKKNDALFVCGTNAFNPSRNPKMDTLEPGDEFSGMARCPTYDAKHANVALFADG 180
Db 124 IKVLLKKNDALFVCGTNAFNPSRNPKMDTLEPGDEFSGMARCPTYDAKHANVALFADG 183

Qy 181 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHD SKWLKEPYFVQAVDYGDIYFFFREIA 240
Db 184 KLYSATVTDFAIDAVIYRSLGESPTLRTVKHD SKWLKEPYFVQAVDYGDIYFFFREIA 243

Qy 241 VEYNTMGKVVFPRAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
Db 244 VEYNTMGKVVFPRAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 303

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
Db 304 DVIRIKGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 363

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFRLTMVRYRL 420
Db 364 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFRLTMVRYRL 423

Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNSEKSYD 480
Db 424 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNSEKSYD 483

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKKTCIASRDPYCGWIKEGG 540
Db 484 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKKTCIASRDPYCGWIKEGG 543

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQEYESR 600
|||||||||||||||||||||||||||||

Db 544 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN----- 579
 Qy 601 GGMLDWKHLKDSPSTDPLGAVSSHNDKKGVIRESYLKGDQLVPVTLLAIAVILAFV 660
 |||||||
 Db 580 -----GVIRESYLKGDQLVPVTLLAIAVILAFV 608
 |||||||
 Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSVTLSGLFGDTQSKDPKPE 720
 |||||||
 Db 609 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSVTLSGLFGDTQSKDPKPE 668
 |||||||
 Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERN 780
 |||||||
 Db 669 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERN 728
 |||||||
 Qy 781 QNLINACTKDMPPMGS PVI PTDLPLRASP SHIPS VVVL PITQQGYQHEYVDQPKMSEVAQ 840
 |||||||
 Db 729 QNLINACTKDMPPMGS PVI PTDLPLRASP SHIPS VVVL PITQQGYQHEYVDQPKMSEVAQ 788
 |||||||
 Qy 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
 |||||||
 Db 789 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 848
 |||||||
 Qy 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLSRNQSFGRGDNP 960
 |||||||
 Db 849 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLSRNQSFGRGDNP 908
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 Qy 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS 1020
 |||||||
 Db 909 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS 968
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 Qy 1021 TSMKPNDACT 1030
 |||||||
 Db 969 TSMKPNDACT 978

RESULT 14
 US-10-449-548-30
 ; Sequence 30, Application US/10449548
 ; Publication No. US20040018977A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alvarez, Enrique
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Dhanabal, Mohanraj
 ; APPLICANT: Khramtsov, Nikolai V.
 ; APPLICANT: LaRochelle, William J.
 ; APPLICANT: Li, Li
 ; APPLICANT: Lichenstein, Henri
 ; APPLICANT: Ooi, Chean Eng
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Zhong, Mei
 ; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
 ; FILE REFERENCE: 15966-540CIP2
 ; CURRENT APPLICATION NUMBER: US/10/449,548
 ; CURRENT FILING DATE: 2003-05-30
 ; PRIOR APPLICATION NUMBER: 09/520,781
 ; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 30
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-30

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Query Match          93.8%; Score 5113.5; DB 15; Length 981;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 1; Indels 55; Gaps 1;

Qy      1 MRSEALLLYFTLLHFAGAGFPEDSEPISHGNYTKQYPFVGHKPGRNTTQRHRLDIQM 60
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4 MRSEALLLYFTLLHFAGAGFPEDSEPISHGNYTKQYPFVGHKPGRNTTQRHRLDIQM 63

Qy      61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGKHDECHNF 120
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      64 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGKHDECHNF 123

Qy      121 IKVLLKKNDDALFVCGTNAFNPSERNYKMDTLEPFGDEFSGMARCPTYDAKHANVALFADG 180
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      124 IKVLLKKNDDALFVCGTNAFNPSERNYKMDTLEPFGDEFSGMARCPTYDAKHANVALFADG 183

Qy      181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHD SKWLKEPYFVQAVDYGDIYFFFREIA 240
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      184 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHD SKWLKEPYFVQAVDYGDIYFFFREIA 243

Qy      241 VEYNTMGKVVFPRAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      244 VEYNTMGKVVFPRAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 303

Qy      301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      304 DVIRIKGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 363

Qy      361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      364 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 423

```

Qy	421	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD	480
Db	424	TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD	483
Qy	481	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGCKKTCIASRDPYCGWIKEGG	540
Db	484	GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGCKKTCIASRDPYCGWIKEGG	543
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESR	600
Db	544	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	579
Qy	601	GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLQLPVVTLLAIAVILA	660
Db	580	-----GVIRESYLKGHDLQLPVVTLLAIAVILA	608
Qy	661	MGAVFSGITVYCVCDHRRKDVAVQRKEKELTHSRRGSMSVTLSGLFGDTQSKDPKPE	720
Db	609	MGAVFSGITVYCVCDHRRKDVAVQRKEKELTHSRRGSMSVTLSGLFGDTQSKDPKPE	668
Qy	721	AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERN	780
Db	669	AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERN	728
Qy	781	QNLINACTKDMPPMGSPVIPTDPLRASPShIPSVVLPITQQGYQHEYVDQPKMSEVAQ	840
Db	729	QNLINACTKDMPPMGSPVIPTDPLRASPShIPSVVLPITQQGYQHEYVDQPKMSEVAQ	788
Qy	841	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDLPPKVPQREASLGPPGASLSQTGL	900
Db	789	MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDLPPKVPQREASLGPPGASLSQTGL	848
Qy	901	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSHLSRNQSFGRGDNPP	960
Db	849	SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSHLSRNQSFGRGDNPP	908
Qy	961	PAPQRVDISIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPLKPDVPPKPSFAPLS	1020
Db	909	PAPQRVDISIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPLKPDVPPKPSFAPLS	968
Qy	1021	TSMKPNDACT 1030	
Db	969	TSMKPNDACT 978	

RESULT 15

US-10-403-676-46

```
; Sequence 46, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
```

; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaoja
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 46
; LENGTH: 971
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-46

Query Match 93.8%; Score 5109.5; DB 12; Length 971;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 970; Conservative 1; Mismatches 0; Indels 59; Gaps 1;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISISHGNYTKQYPFVGHKPGRNTTQRHRLDIQM 60
Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISISHGNYTKQYPFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120
Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120

Qy 121 IKVLLKKNDALFVCGTNAFNPSCKNYKMDTLEPFGDEFSGMARCPTYDAKHANVALFADG 180
Db 121 IKVLLKKNDALFVCGTNAFNPSCKNYKMDTLEPFGDEFSGMARCPTYDAKHANVALFADG 180

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240
Db 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240

Qy 241 VEYNTMGKVVFPRAVQCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
Db 241 VEYNTMGKVVFPRAVQCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
Db 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

Qy 361 VPKRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 420
Db 361 VPKRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR--- 417

Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYD 480
Db 418 -----CSYD 421

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 540
Db 422 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 481

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESR 600
Db 482 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESR 541

Qy 601 GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGDQLVPVTLLAIAVILAFV 660
Db 542 GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGDQLVPVTLLAIAVILAFV 601

Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSQLFGDTQSKDPKPE 720
Db 602 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSQLFGDTQSKDPKPE 661

Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGREWERN 780
Db 662 AILTPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGREWERN 721

Qy 781 QNLINACTKDMPPMGSPVIPTDLPLRASPShIPSVVLPITQQGYQHEYVDQPKMSEVAQ 840

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
722 QNLINACTKDMPPMGSPIPTDLPLRASPSHIPSVVVLPIQQGYQHEYVDQPKMSEVAQ 781

QY 841 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 782 MALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGL 841

QY 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSSLRNQSFGRGDNPP 960
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 842 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSSLRNQSFGRGDNPP 901

QY 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKDVPFPKPSFAPLS 1020
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 902 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKDVPFPKPSFAPLS 961

QY 1021 TSMKPNDACT 1030
| | | | | | | |
Db 962 TSMKPNDACT 971

Search completed: March 24, 2004, 13:19:31
Job time : 77.7731 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 24, 2004, 13:11:03 ; Search time 71.9691 Seconds
(without alignments)
4515.598 Million cell updates/sec

Title: US-09-856-681A-2

Perfect score: 5450

Sequence: 1 MRSEALLLYFTLLHFAGAGE.....PPKPSFAPLSTS MKPNDACT 1030

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database : SPTREMBL_25:*  
1: sp_archea:/*  
2: sp_bacteria:/*  
3: sp_fungi:/*  
4: sp_human:/*  
5: sp_invertebrate:/*  
6: sp_mammal:/*  
7: sp_mhc:/*  
8: sp_organelle:/*  
9: sp_phage:/*  
10: sp_plant:/*  
11: sp_rat:/*  
12: sp_virus:/*  
13: sp_vertebrate:/*  
14: sp_unclassified:/*  
15: sp_rvirus:/*  
16: sp_bacterioplasm:/*  
17: sp_archeap:/*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

1	5024.5	92.2	1005	11	Q9EQ71	Q9eq71 mus musculu
2	3677	67.5	699	4	Q96SW4	Q96sw4 homo sapien
3	2980.5	54.7	574	4	Q96SM8	Q96sm8 homo sapien
4	2963	54.4	587	11	Q8BUT0	Q8but0 mus musculu
5	2961	54.3	605	11	Q8BXZ7	Q8bxz7 mus musculu
6	2952	54.2	562	4	Q96SY4	Q96sy4 homo sapien
7	2947	54.1	562	4	Q8NC49	Q8nc49 homo sapien
8	2621.5	48.1	507	4	Q96T04	Q96t04 homo sapien
9	2368	43.4	1073	4	Q8NFY4	Q8nfy4 homo sapien
10	2349	43.1	1017	4	Q8NFY5	Q8nfy5 homo sapien
11	2315.5	42.5	998	4	Q8NFY6	Q8nfy6 homo sapien
12	2314	42.5	1011	4	Q8NFY3	Q8nfy3 homo sapien
13	2314	42.5	1022	4	Q9P249	Q9p249 homo sapien
14	2309.5	42.4	1009	11	Q80TD0	Q80td0 mus musculu
15	2213	40.6	418	4	Q96JU9	Q96ju9 homo sapien
16	1908.5	35.0	595	11	Q8BKG8	Q8bkg8 mus musculu
17	1876.5	34.4	687	4	Q9BXR8	Q9bxr8 homo sapien
18	1611	29.6	476	4	Q8NFY7	Q8nfy7 homo sapien
19	1526.5	28.0	963	11	Q91Y36	Q91y36 mus musculu
20	1480.5	27.2	452	13	Q7T165	Q7t165 brachydanio
21	1386.5	25.4	367	4	Q9HAH9	Q9hah9 homo sapien
22	1355.5	24.9	923	11	Q8R4U3	Q8r4u3 mus musculu
23	1320	24.2	920	11	Q8R4U4	Q8r4u4 rattus norv
24	1059	19.4	366	13	Q7ZV83	Q7zv83 brachydanio
25	856.5	15.7	770	5	Q44253	Q44253 drosophila
26	854.5	15.7	770	5	Q9V3M4	Q9v3m4 drosophila
27	847.5	15.6	774	13	Q8JIW9	Q8jiw9 xenopus lae
28	823.5	15.1	844	11	Q8BXU8	Q8bxu8 mus musculu
29	817.5	15.0	748	4	Q8TB71	Q8tb71 homo sapien
30	802.5	14.7	777	11	Q8BMF6	Q8bmf6 mus musculu
31	802.5	14.7	777	11	Q8BH34	Q8bh34 mus musculu
32	779.5	14.3	724	5	Q9V7Q7	Q9v7q7 drosophila
33	771	14.1	1122	11	Q7TT33	Q7tt33 mus musculu
34	768	14.1	697	5	Q8MLF1	Q8mlf1 drosophila
35	763	14.0	635	4	Q96GX0	Q96gx0 homo sapien
36	749	13.7	756	13	Q8QGU9	Q8qgu9 gallus gall
37	748	13.7	775	11	Q9QX23	Q9qx23 mus musculu
38	736.5	13.5	799	11	Q8BJC1	Q8bjc1 mus musculu
39	735.5	13.5	862	4	Q7Z5S4	Q7z5s4 homo sapien
40	694.5	12.7	616	5	Q9V7P8	Q9v7p8 drosophila
41	693	12.7	963	4	Q9C0C4	Q9c0c4 homo sapien
42	686	12.6	782	4	Q9NS98	Q9ns98 homo sapien
43	666.5	12.2	1083	5	Q9VTTO	Q9vtt0 drosophila
44	666.5	12.2	1091	5	Q7YU67	Q7yu67 drosophila
45	660	12.1	823	11	Q8BIR6	Q8bir6 mus musculu

ALIGNMENTS

RESULT 1

Q9EQ71

ID Q9EQ71 PRELIMINARY; PRT; 1005 AA.
AC Q9EQ71;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Axon guidance signal SEMA6A1.
 GN SEMA6A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20564339; PubMed=10993894;
 RA Klostermann A., Lutz B., Gertler F., Behl C.;
 RT "The orthologous human and murine semaphorin 6A-1 proteins (SEMA6A-1/Sema6A-1) bind to the Enabled/Vasodilator-stimulated Phosphoprotein-like Protein (EVL) via a novel carboxyl-terminal Zyxin-like domain.";
 RL J. Biol. Chem. 275:39647-39653(2000).
 DR EMBL; AF288666; AAG29494.1; -.
 DR MGD; MGI:1203727; Sema6a.
 DR GO; GO:0016021; C:integral to membrane; ISS.
 DR GO; GO:0008580; F:cytoskeletal regulator activity; ISS.
 DR GO; GO:0007411; P:axon guidance; ISS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; ISS.
 DR GO; GO:0007399; P:neurogenesis; ISS.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 SQ SEQUENCE 1005 AA; 111758 MW; 57B69927F45B079D CRC64;

Query Match 92.2%; Score 5024.5; DB 11; Length 1005;
 Best Local Similarity 91.9%; Pred. No. 0;
 Matches 948; Conservative 26; Mismatches 30; Indels 27; Gaps 2;

Qy	1 MRSEALLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Db	1 MRPAALLLCCLLHCAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM	60
Qy	61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF	120
	:	
Db	61 IMIMNRTLYVAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF	120
Qy	121 IKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPGDEFSGMARCPTYDAKHANVALFADG	180
	:	
Db	121 IKVLLKKNDTFLVCGTNAFNPSCRNYRVDTLETFGDEFSGMARCPTYDAKHVNIALFADG	180
Qy	181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA	240
Db	181 KLYSATVTDFLAIDAVIYRSPGDSPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA	240
Qy	241 VEYNTMGKVVFPRVAQVCKNDMGGSORVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Db	241 VEYNTMGKVVFPRVAQVCKNDMGGSORVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT	300
Qy	301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIADVFTGRFKEQKSPDSTWTPVPDER	360

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
 |||||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:
 Db 361 VPKPRPGCCAGSSLEKYATSNEFPDDTLNFIKTHPLMDEAVPSIINRPWFLRTMVRYRL 420

 Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLFEEMSVYNSEKCSYD 480
 |||||:||||||:||||||:
 Db 421 TKIAVDNAAGPYQNHTVV-----FLEEMNVYNPEKCSYD 454

 Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG 540
 |||||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:
 Db 455 GVEDKRIMGMQLDRASGSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWVRESG 514

 Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESR 600
 :|:|||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:
 Db 515 SCAHLSPSRLTFEQDIERGNTDGLGDCHNSFVALNGHASSLYPNTTSDSASRDGYESR 574

 Qy 601 GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLGHDQLVPVTLLAIAVILA 660
 |||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:
 Db 575 GGMLDWNDLLEAPGSTDPLGAVSSHNHQDKKGVIRESYLSNDQLVPVTLLAIAVILA 634

 Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSVTKLSQLFGDTQSKDPKPE 720
 |||||||:||||||:||||||:||||||:||||||:||||||:||||||:
 Db 635 MGAVFSGIIVYCVCDHRRKDVAVVRKEKELTHSRRGSMSVSELSQLFGDTQSKDPKPE 694

 Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGREWERN 780
 |||||||:||||||:||||||:||||||:||||||:||||||:
 Db 695 AILTPLMHNGKLATSSNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPNRGREWERN 754

 Qy 781 QNLINACTKDMPPMGSPVIPTDLPLRASPShIPSvvLPITQQGYQHEYVDQPKMSE-VA 839
 ||:|||||:||||||:||||||:||||||:||||||:||||||:
 Db 755 QNIINACTKDMPPMGSPVIPTDLPLRASPShIPSvvLPITQQGYQHEYVDQPKMSEVVA 814

 Qy 840 QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTG 899
 |||||||:||||||:||||||:||||||:||||||:||||||:
 Db 815 QMALEDQAATLEYKTTKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGTSLSQTG 874

 Qy 900 LSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSSLRNQSFGRGDNP 959
 |||||||:||||||:||||||:||||||:||||||:
 Db 875 LSKRLEMQHSSSYGLEYKRSYPTNSLTRSHQTTLKRNNTNSSNSSLRNQSFGRGDNP 934

 Qy 960 PPAPQRVDISIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKDVPKKPSFAPL 1019
 |||||||:||||||:||||||:||||||:||||||:
 Db 935 PPAPQRVDISIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKDVPKKPSFAPL 994

 Qy 1020 STSMKPNDACT 1030
 |||||||:
 Db 995 STSMKPNDACT 1005

RESULT 2

Q96SW4

ID Q96SW4 PRELIMINARY; PRT; 699 AA.

AC Q96SW4;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein FLJ14595.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK027501; BAB55158.1; -.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 699 AA; 76723 MW; 2E5F111D59741394 CRC64;

Query Match 67.5%; Score 3677; DB 4; Length 699;
 Best Local Similarity 100.0%; Pred. No. 4.5e-291;
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	332	MLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF	391
Db	1	MLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNF	60
Qy	392	IKTHPLMDEAVPSIFNRPWFRLTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFL	451
Db	61	IKTHPLMDEAVPSIFNRPWFRLTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKFL	120
Qy	452	ARIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP	511
Db	121	ARIGNSGFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVP	180
Qy	512	LGRCERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS	571
Db	181	LGRCERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNS	240
Qy	572	FVALNGHSSLLPSTTSSTAQEYESRGMLDWKHLLDSPDSTDPLGAVSSHNDQDKK	631
Db	241	FVALNGHSSLLPSTTSSTAQEYESRGMLDWKHLLDSPDSTDPLGAVSSHNDQDKK	300
Qy	632	GVIRESYLKGHHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKEL	691
Db	301	GVIRESYLKGHHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKEL	360
Qy	692	THSRRGSMSSVTKLSQLFGDTQSKEPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLD	751
Db	361	THSRRGSMSSVTKLSQLFGDTQSKEPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLD	420
Qy	752	LTALPTPESTPTLQQKRKPSRGSREWERNQNLIINACTKDMPPMGSPVIPTDLPLRASPSH	811

Db	421	LTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPIPTDPLPLRASPSH	480
Qy	812	IPSVVVLPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV	871
Db	481	IPSVVVLPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV	540
Qy	872	ENLDLPPKVPQREASLGPPGASILSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA	931
Db	541	ENLDLPPKVPQREASLGPPGASILSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQA	600
Qy	932	TTLKRNNNTNSSNSSLRNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNA	991
Db	601	TTLKRNNNTNSSNSSLRNQSFGRGDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNA	660
Qy	992	YNSLTRSGLKRTPSLKDVPVPPKPSFAPLSTMKPNDACT	1030
Db	661	YNSLTRSGLKRTPSLKDVPVPPKPSFAPLSTMKPNDACT	699

RESULT 3

Q96SM8

ID Q96SM8 PRELIMINARY; PRT; 574 AA.
AC Q96SM8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein FLJ14748.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK027654; BAB55269.1; -.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR SMART; SM00423; PSI; 1.
KW Hypothetical protein.
SQ SEQUENCE 574 AA; 62822 MW; 0C79E01A4117A495 CRC64;

Query Match 54.7%; Score 2980.5; DB 4; Length 574;
Best Local Similarity 90.7%; Pred. No. 2.5e-234;
Matches 574; Conservative 0; Mismatches 0; Indels 59; Gaps 1;

Qy	398	MDEAVPSIFNRPWFLRTMVRYLTKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNS	457
Db	1	MDEAVPSIFNRPWFLRTMVR-----	20

Qy 458 GFLNDSLFLLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CER 517
 |||||||
 Db 21 -----CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGR CER 61
 |||||||
 Qy 518 HGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLT FEQDIERGNTDGLGDCHNSFVALNG 577
 |||||||
 Db 62 HGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLT FEQDIERGNTDGLGDCHNSFVALNG 121
 |||||||
 Qy 578 HSSSLPSTTSYSTAQEGYESRGGM DWKHLLDSPDSTDPLGA VSSHNHQDKKGVIRES 637
 |||||||
 Db 122 HSSSLPSTTSYSTAQEGYESRGGM DWKHLLDSPDSTDPLGA VSSHNHQDKKGVIRES 181
 |||||||
 Qy 638 YLK GH DQLVPVTLLAI A VILA FVMGA VFS GITVY CVCDHRRKDVA VVQRKE KELTHS RRG 697
 |||||||
 Db 182 YLK GH DQLVPVTLLAI A VILA FVMGA VFS GITVY CVCDHRRKDVA VVQRKE KELTHS RRG 241
 |||||||
 Qy 698 SMSSVTKLSGLFGDTQS KDPKPEA ILT P LHMNGKLATPGNTAKMLI KADQHHL DL TALPT 757
 |||||||
 Db 242 SMSSVTKLSGLFGDTQS KDPKPEA ILT P LHMNGKLATPGNTAKMLI KADQHHL DL TALPT 301
 |||||||
 Qy 758 PESTPTLQQKRKP SRGSREWERNQN LINACTKDMPPM GSPV I PTDLPLRASP SHIPS VVV 817
 |||||||
 Db 302 PESTPTLQQKRKP SRGSREWERNQN LINACTKDMPPM GSPV I PTDLPLRASP SHIPS VVV 361
 |||||||
 Qy 818 LPITQQGYQHEYVDQPKM SEVAQMALEDQAATLEYKT I KEHLSSKSPN HGVNL VENLDSL 877
 |||||||
 Db 362 LPITQQGYQHEYVDQPKM SEVAQMALEDQAATLEYKT I KEHLSSKSPN HGVNL VENLDSL 421
 |||||||
 Qy 878 PPKVPQREASLGPPGASLSQTGLSKRLEMHSSSYGV DYKRSYPTNSL TRSHQATT LKRN 937
 |||||||
 Db 422 PPKVPQREASLGPPGASLSQTGLSKRLEMHSSSYGV DYKRSYPTNSL TRSHQATT LKRN 481
 |||||||
 Qy 938 NTNSSNSHLSRNQSFGRGDNP PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR 997
 |||||||
 Db 482 NTNSSNSHLSRNQSFGRGDNP PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTR 541
 |||||||
 Qy 998 SGLKRTPSLKP DVPPKPSFAPLSTS MKPND ACT 1030
 |||||||
 Db 542 SGLKRTPSLKP DVPPKPSFAPLSTS MKPND ACT 574

RESULT 4

Q8BUTO

ID Q8BUTO PRELIMINARY; PRT; 587 AA.
 AC Q8BUTO;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sema domain.
 GN A730020P05RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK082711; BAC38582.1; -.
 DR MGD; MGI:2443196; A730020P05Rik.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00630; Sema; 1.
 SQ SEQUENCE 587 AA; 66044 MW; EB9C7B102C4DB97A CRC64;

Query Match 54.4%; Score 2963; DB 11; Length 587;
 Best Local Similarity 95.1%; Pred. No. 7e-233;
 Matches 549; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MRSEALLLYFTLLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
 || |||| ||||| |||||||||||||||||||||||||||||||||||||||
 Db 1 MRPAALLCLTLHCAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120
 ||||| ||||:|||||||||||||||||||||||||||||||||||||
 Db 61 IMIMNRTLYVAARDHIYTVDIDTSHTEEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120

Qy 121 IKVLLKKNDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCPTYDAKHANVALFADG 180
 ||||||| ||||||| ||||||| :||||| ||||||| ||||||| :|||||
 Db 121 IKVLLKKNDALFVCGTNAFNPSCKNYRVDTLETFGDEFSGMARCPTYDAKHANIALFADG 180

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFREIA 240
 ||||||| ||||||| :||||| ||||||| ||||||| ||||||| |||||||
 Db 181 KLYSATVTDFLAIDAVIYRSLGDSPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFREIA 240

Qy 241 VEYNTMGKVVFPRAQVCKNDMGGSQLKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 241 VEYNTMGKVVFPRAQVCKNDMGGSQLKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
 ||||||| ||||||| ||||||| ||||||| :||||| ||||||| |||||||
 Db 301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIANVFTGRFKEQKSPDSTWTPVPDER 360

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
 ||||||| ||||||| :||||| ||||||| ||||||| |||||||
 Db 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIINRPWFLRTMVRYRL 420

Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD 480
 ||||||| ||||||| ||||||| ||||||| :||||| ||||||| :||| |||||||
 Db 421 TKIAVDNAAGPYQNHTVVFLGSEKGIIILKFLARIGSSGFLNGSLFLEEMNVYNPEKCSYD 480

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKKTCIASRDPYCGWIKEGG 540
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| :|||
 Db 481 GVEDKRIMGMQLDRASGSLYVAFSTCVIKVPLGRCEHGKCKKTCIASRDPYCGWVRESG 540

Qy 541 ACSHLSPLSRLTFEQDIERGNTDGLGDCHNSFVALNG 577
 :||| ||||||| ||||||| ||||||| |||||||
 Db 541 SCAHLSPLSRLTFEQDIERGNTDGLGDCHNSFVALNG 577

RESULT 5

Q8BXZ7

ID Q8BXZ7 PRELIMINARY; PRT; 605 AA.
AC Q8BXZ7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sema domain.
GN A730020P05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK042751; BAC31351.1; -.
DR MGD; MGI:2443196; A730020P05Rik.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00630; Sema; 1.
SQ SEQUENCE 605 AA; 68299 MW; B4FE713BE8AF6E90 CRC64;

Query Match 54.3%; Score 2961; DB 11; Length 605;
Best Local Similarity 94.5%; Pred. No. 1.1e-232;
Matches 550; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 60
|| ||||| ||||| |||||||||||||||||||||||||||||||||||||||
Db 1 MRPAALLLCLLHCAGAGFPEDSEPISHGNYTKQYPVFGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120
||||| ||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 IMIMNRTLYVAARDHIYTVDIDTSHTEIYCSKKLTWKSQADVDTCRMKGKHKDECHNF 120

Qy 121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPFGDEFSGMARCPYDAKHANVALFADG 180
||||| ||||| ||||| ||||| ||||| :||| ||||| ||||| ||||| :||| |||||
Db 121 IKVLLKKNDTFLVCGTNAFNPSCKNYRVDTLETFGDEFSGMARCPYDAKHANIALFADG 180

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240
||||| ||||| ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 KLYSATVTDFLAIDAVIYRSLGDSPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIA 240

Qy 241 VEYNTMGKVVFPRVAQVCKNDMGGSQLKEQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 VEYNTMGKVVFPRVAQVCKNDMGGSQLKEQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLIASVFTGRFKEQKSPDSTWTPVPDER 360
||||| ||||| ||||| ||||| ||||| ||||| :||| ||||| ||||| |||||

Db 301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIANVFTGRFKEQKSPDSTWTPVPDER 360
 Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 361 VPKPRPGCCAGSSLEKYATSNEFPDDTLNFIKTHPLMDEAVPSIINRPWFLRTMVRYRL 420
 Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD 480
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 421 TKIAVDNAAGPYQNHTVVFLGSEKGIIILKFLARIGSSGFLNGSLFLEEMNVNPEKCSYD 480
 Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKKTCIASRDPYCGWIKEGG 540
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 481 GVEDKRIMGMQLDRASGSLYVAFSTCVIKVPLGRcerHGKCKKTCIASRDPYCGWVRESG 540
 Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSL 582
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 541 SCAHLSPLSRLTFEQDIERGNTDGLGDCHNSFVALNDISTPL 582

RESULT 6

Q96SY4

ID Q96SY4 PRELIMINARY; PRT; 562 AA.
 AC Q96SY4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein FLJ14565.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK027471; BAB55136.1; -.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003659; Plexin-like.
 DR SMART; SM00423; PSI; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 562 AA; 61313 MW; 6AB3685FAD1DD78A CRC64;

Query Match 54.2%; Score 2952; DB 4; Length 562;
 Best Local Similarity 100.0%; Pred. No. 5.2e-232;
 Matches 562; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 469 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKKTCIAS 528
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKKTCIAS 60

Qy	529	RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTT	588
Db	61	RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTT	120
Qy	589	SDSTAQEYESRGGMULDWKHLLDSPDSTDPLGAVSSHNDQKKGVIRESYLKGDQLVPV	648
Db	121	SDSTAQEYESRGGMULDWKHLLDSPDSTDPLGAVSSHNDQKKGVIRESYLKGDQLVPV	180
Qy	649	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVQRKEKELTHSRRGSMSSVTKLSGL	708
Db	181	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVQRKEKELTHSRRGSMSSVTKLSGL	240
Qy	709	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLTLALPTPESTPTLQQKR	768
Db	241	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLTLALPTPESTPTLQQKR	300
Qy	769	KPSRGSREWERNQNLINACTKDMPPMGSPIPTDLPLRASPShIPSVVVLPIQQGYQHE	828
Db	301	KPSRGSREWERNQNLINACTKDMPPMGSPIPTDLPLRASPShIPSVVVLPIQQGYQHE	360
Qy	829	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDLPPKVPQREASL	888
Db	361	YVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDLPPKVPQREASL	420
Qy	889	GPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLS	948
Db	421	GPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLS	480
Qy	949	RNQSFGRGDNPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLP	1008
Db	481	RNQSFGRGDNPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLP	540
Qy	1009	DVPPKPSFAPLSTMKPNDACT	1030
Db	541	DVPPKPSFAPLSTMKPNDACT	562

RESULT 7

Q8NC49

ID Q8NC49 PRELIMINARY; PRT; 562 AA.
 AC Q8NC49;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ90494.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahashi K.,
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 RT "NEDO human cDNA sequencing project.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK074975; BAC11326.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 562 AA; 61286 MW; 708041459E34D78A CRC64;

 Query Match 54.1%; Score 2947; DB 4; Length 562;
 Best Local Similarity 99.8%; Pred. No. 1.3e-231;
 Matches 561; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 469 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKKTCIAS 528
 |||||||
 Db 1 MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKKTCIAS 60

 Qy 529 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTT 588
 |||||||
 Db 61 RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTT 120

 Qy 589 SDSTAQEYESRGGMMDWKHLLSPDSTDPLGAVSSHNDQDKKGVIRESYLGHDQLVPV 648
 |||||||
 Db 121 SDSTAQEYESRGGMMDWKHLLSPDSTDPLGAVSSHNDQDKKGVIRESYLGHDQLVPV 180

 Qy 649 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGL 708
 |||||||
 Db 181 TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGL 240

 Qy 709 FGDTQS KDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKR 768
 |||||||
 Db 241 FGDTQS KDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKR 300

 Qy 769 KPSRGSREWERNQNLI NACTKDMP PMGSPV IPTDLPLRASP SHIPS VVLP ITQQGYQHE 828
 |||||||
 Db 301 KPSRGSREWERNQNLI NACTKDMP PMGSPV IPTDLPLRASP SHIPS VVLP ITQQGYQHE 360

 Qy 829 YVDQPKMSEVAQMALEDQAATLEYKTIKEH LSSKSPN HGVNLVENLDSLPPKVPQREASL 888
 |||||||
 Db 361 YVDQPKMSEVAQMALEDQAATLEYKTIKEH LSSKSPN HGVNLVENLDSLPPKVPQREASL 420

 Qy 889 GPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLS 948
 |||||||
 Db 421 GPPGASLSQTGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLS 480

 Qy 949 RNQS FGRGDNP PPA PQRV DSIQV HSSQ PGSQ AVTV SRQPSLNAY NSL TRS GLK RTP S LKP 1008
 |||||:
 Db 481 RNQS FGRGDNP PPA PQRV DSIQV HSSQ PGSQ AVTV SRQPSLNAY NSL TRS GLK RTP S LKP 540

 Qy 1009 DVPPKPSFAPLSTS MKPND ACT 1030
 |||||||
 Db 541 DVPPKPSFAPLSTS MKPND ACT 562

RESULT 8

Q96T04

ID Q96T04 PRELIMINARY; PRT; 507 AA.
 AC Q96T04;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein FLJ14533.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK027439; BAB55111.1; -.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003659; Plexin-like.
 DR SMART; SM00423; PSI; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 507 AA; 55464 MW; 8CC567B438C51B39 CRC64;

Query Match 48.1%; Score 2621.5; DB 4; Length 507;
 Best Local Similarity 90.2%; Pred. No. 4.3e-205;
 Matches 507; Conservative 0; Mismatches 0; Indels 55; Gaps 1;

Qy	469	MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKKTCIAS	528
Db	1	MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKKTCIAS	60
Qy	529	RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTT	588
Db	61	RDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALN-----	108

Qy	589	SDSTAQEYESRGGMULDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLGHDQLVPV	648
Db	109	-----GVIRESYLGHDQLVPV	125

Qy	649	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGL	708
Db	126	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGL	185
Qy	709	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKR	768
Db	186	FGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKR	245
Qy	769	KPSRGSREWERNQNLIINACTKDMPPMGSPVIPTDLPLRASPSPHIPSVVVLPIQQGYQHE	828
Db	246	KPSRGSREWERNQNLIINACTKDMPPMGSPVIPTDLPLRASPSPHIPSVVVLPIQQGYQHE	305
Qy	829	YVDQPKMSEVAQMALEDQAATLEYKTIKEHSSKSPNHGVNLVENLDSLPPKVPQREASL	888
Db	306	YVDQPKMSEVAQMALEDQAATLEYKTIKEHSSKSPNHGVNLVENLDSLPPKVPQREASL	365
Qy	889	GPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTIKNNTNSSNSSLHS	948

Db 366 GPPGASILSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSSLHS 425
Qy 949 RNQSFGRGDNPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 1008
|||
Db 426 RNQSFGRGDNPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP 485
|||
Qy 1009 DVPPKPSFAPLSTSMKPNDACT 1030
|||
Db 486 DVPPKPSFAPLSTSMKPNDACT 507

RESULT 9

Q8NFY4

ID Q8NFY4 PRELIMINARY; PRT; 1073 AA.
AC Q8NFY4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Semaphorin 6D isoform 4.
GN SEMA6D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Qu X., Zhai Y., Wei H., Yu Y., Tang F., He F.;
RT "Homo sapiens semaphorin 6D isoform 4 (SEMA6D.4) mRNA, complete cds.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF389429; AAM69452.1; -.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00630; Sema; 1.
SQ SEQUENCE 1073 AA; 119872 MW; 7DCE4DFC5BF70F9E CRC64;

Query Match 43.4%; Score 2368; DB 4; Length 1073;
Best Local Similarity 46.0%; Pred. No. 7.5e-184;
Matches 512; Conservative 159; Mismatches 308; Indels 134; Gaps 30;

Qy 1 MRSEALLLYFTLL---HFAGAGFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQRHRLD 57
|| | | || ||| ||:: :|::||||| | :| | :| |||||
Db 1 MRVFLLCAYILLLMVSQLRAVSFPEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLD 58
|||
Qy 58 IQMIMIMNGTLYIAARDHIYTVDIDTSHTEIYCSKKLTWKSQADVDTCRMKGHKDEC 117
|::: : ||||| || :|||::: |: :|||||:||| | :| | |||||||
Db 59 FQLMLKIRDTLYIAGRQVYTVNLNEMPKTEVIPNKKLTWRSRQQDRENCAMKGHKDEC 118
|||
Qy 118 HNFIKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCPYDAKHANVALF 177
||||| : :||: :||||||| || |:: ||| |:| ||:|||:||: ||||||
Db 119 HNFIKVVFVPRNDEMVFVCGTNAFPNCMCRYRLSTLEYDGEIISGLARCPFDARQTNVALF 178
|||
Qy 178 ADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFF 237
||||||| | ||| |||||||:|: | ||:|:|||:|||:|: |::|:|:|:|||
Db 179 ADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIYEYGNVYFFF 238
|||
Qy 238 EIAVEYNTMGKVVPRVAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGDSHFYFNILQ 297

Db |||||:| :|| |: |||:||||||||| ||||| ||||| ||||| :|||
239 EIAVEHNNLKGAVYSRVARICKNDMGGSGRVLEKHWTSLKARLNCSVPGDSFFYFDVLQ 298

Qy 298 AVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
::|:|:|:||| |: |: ||| |||: | || || ||| |||:||| |||
Db 299 SITDIIQINGIPTVVGVFTTQLNSIPGSAVCAFSMDDIEKVFKGRFKEQKTPDSVWTAVP 358

Qy 358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
:::|:||||| | | || :|||:||:||:||| ||| | :||| :| |||
Db 359 EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSFIKSHPLMDSAVPIADEPWFTKTRVR 418

Qy 418 YRLTKIAVDTAAGPYQNHTVFLGSEKGIILKFLARIGNSGF-LNDSLFLLEMSVYNSEK 476
|||| |:|| :|||||:|||:||| |:|| | | |||: |||: ||| |
Db 419 YRLTAISVDHSAGPYQNYTVIFVGSEAGMVLKVLAK--TSPFSLNDSVLLEEAYNHAK 476

Qy 477 CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGCKKTCIASRDPYCGWI 536
|| : |||::: :|||: :|||||:||:|| | |||:||| |||:|||||:
Db 477 CSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERYGSCKKSCIASRDPYCGWL 536

Qy 537 KEGGACSHLSPNSRLT-FEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQE 595
: |:| ::| :||| | ||| | |||| | :||:|| |
Db 537 SQ-GSCGRVTPGMLAEGYEQDTEFGNTAHLGDCH-----EILPTSTTPD---- 579

Qy 596 GYESRGG-----MLD-WKHLL-----DSP---DSTDP 618
|: | | | | | | | | | | | | | | | | | | | | | | | | |
Db 580 -YKIFGGPTSDMEVSSSVTTMASIPEITPKVIDTWRPKLTSSRKFVVQDDPNTSDFTDP 638

Qy 619 LGAVSSHNHQDKKGVIRESYLGHDQLPVTLAIAVILAFAVMGAVFSGITVYCVCD-HR 677
| : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 639 LSGI-----PKGVRWEVQSGESNQMVHMNVLITCVFAAFVLGAFIAGVAVCYRDMFV 691

Qy 678 RKDVAVVQRKEKELTHSRGSMSSVTKLSGLFG---DTQSKDPKPEAILTPLMHNGKLA 733
||: | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 692 RKNRKI--HKDAESAQSCTDSSGSFAKLNGLFDSPVKEYQQNIDSPKLYSNLLTSRKELP 749

Qy 734 TPGNTAKMLIKADQHLDLTALPTPESTPTLQQKRKPSRGREWERNQNLINACTKDMPP 793
|:| |::| :| | | | | | | | | | | | | | | | | | | | | |
Db 750 PNGDTKSMVMDHRGQPPELAALPTPESTPVLHQKTLQAMKSHSEKAHGH--GASRKETPQ 807

Qy 794 MGSPVIPTDLPLRASPISHIPS VVLPITQQGYQHEY-----VDQP---KMS 836
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 808 FFPSSPPPHSPL--SHGHIPSAIVLPNATHDYNTSFNSNAHKAEKKLQNIIDHPLTKSS 865

Qy 837 EVAQMALEDQAATLEYKTIKEHLSSKSPN-----HGVNLVENLDSL---PPKVP 882
| : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 866 KRDHRRSVDNRNTL--NDLLKHLNDPNSNPKAIMGDIQMAHQNLMLDPGMSEVPPKVP 923

Qy 883 QREASLGPPGASLSQTGLSKRLEMHSSSY---GVDYKRSYPTNSLTRSHQATTLKRNNT 939
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 924 NREASLYSPPSTLPRNSPTKRVDVPTTPGVPMTSLERQRGYHKNSSQR-HSISAMPK-NL 981

Qy 940 NSSNSSHLSRNQSFGRGD-NPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-- 996
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 982 NSPNGVLLSRQPSMNRGGYMPTPTGAKVDYI-----GTPVSVHLQPSLSRQSSYTSN 1034

Qy 997 ----RSGLKRTPSLKPVDVPPKPSFAPLSTMKP 1025
|:||||||||||||| | | | | | | | | | | | | | | | | | | | | | |

Db 1035 GTLPRTGLKRTPSLKPDPVPPKPSFVPQTPSVRP 1067

RESULT 10

Q8NFY5

ID Q8NFY5 PRELIMINARY; PRT; 1017 AA.
AC Q8NFY5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Semaphorin 6D isoform 3.
GN SEMA6D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Qu X., Wei H., Zhai Y., Yu Y., Tang F., He F.;
RT "Homo sapiens semaphorin 6D isoform 3 (SEMA6D.3) mRNA, complete cds.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF389428; AAM69451.1; -.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00630; Sema; 1.
SQ SEQUENCE 1017 AA; 113736 MW; 4D639CEBADD9F2A0 CRC64;

Query Match 43.18; Score 2349; DB 4; Length 1017;
Best Local Similarity 46.7%; Pred. No. 2.5e-182;
Matches 503; Conservative 155; Mismatches 302; Indels 116; Gaps 27;

Qy 1 MRSEALLLYFTLL---HFAGAGFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQRHRLD 57
|| | | || ||| ||:: :|::||||| | :| | :| ||||
Db 1 MRVFLLCAYILLLMVSQRLAVSFPEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLD 58

Qy 58 IQMIMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRADVDTCRMKGKHDEC 117
|::: : ||||| || :|||::: | : :|||||:||| | : | |||||||||
Db 59 FQLMLKIRDLYIAGRQVYTVNLNEMPKTEVIPNKKLTWRSRQQDRENCAMKGKHDEC 118

Qy 118 HNFIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALF 177
|||||| : :||: :||||||| || |:: ||| |:: |||:|||:||: |||||
Db 119 HNFIKVFPVRNDEMVFVCGTNAFNPMCRYRLSTLEYDGEISGLARCPFDARQTNVALF 178

Qy 178 ADGKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFF 237
||||||| ||| |||||||:|: |||:|||:|||:||: ||:|||:|||:
Db 179 ADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIIEGNYVYFFF 238

Qy 238 EIAVEYNTMGKVVFPRVAQVCKNDMGGSORVLEKQWTSFLKARLNCSVPGDSHFYFNILQ 297
|||||:| :|| |: |||:||||||||| ||| ||||||| |||:|||
Db 239 EIAVEHNNLGKAVYSRVARICKNDMGGSORVLEKHWTSFLKARLNCSVPGDSFYFDVLQ 298

Qy 298 AVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
::||:||| |: | :| | |||||||: | || | || |||:||| |||
Db 299 SITDIIQINGIPTVVGFTTQLNSIPGSAVCAFSMDDIEKVFGRFKEQKTPDSVWTAVP 358

Qy 358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417

Db	359	EDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSFIKSHPLMDSAVPIADEPWFTRKTRVR	418
Qy	418	YRLTKIAVDTAAGPYQNHTVVFLGSEKGIIKLFLARIGNSGF-LNDSLLEEMSVDNSEK	476
Db	419	YRLTAISVDSAGPYQNYTVIFVGSEAGMVLKVLAKE-TSPFSLNDSVLLEEAYNHAK	476
Qy	477	CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGKCKTCIASRDPYCGWI	536
Db	477	CSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERYGSCKKSCIASRDPYCGWL	536
Qy	537	KEGGACSHLSPNSRLT-FEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQE	595
Db	537	SQ-GSCGRVTPGMLAEGYEQDTEFGNTAHLGDCH-----EILPTSTTPD-----	579
Qy	596	GYESRGGMQLDWKHLLDSPDSTDPLGAVSSHNNHQDKKGVIRESYLGHDQLVPVTLLAAIV	655
Db	580	-YKIFGG-----PTS-----GVRWEVQSGESNQMVHMNVLITCV	612
Qy	656	ILAFVMGAVFSGITVYCVCD-HRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFG----	710
Db	613	FAAFVLGAFIAGVAVCYRDMFVRKNRKI--HKDAESAQSCTDSSGSFAKLNGLFDSPVK	670
Qy	711	DTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKP	770
Db	671	EYQQNIDSPKLYSNLLTSRKELPPNGDTKSMVMDHRGQPPEALALPTPESTPVLHQKTLQ	730
Qy	771	SRGSREWERNQNLINACTKDMPPMGSPVIPTDLPLRASPISHIPSVVVLPITOQQGYQHEY-	829
Db	731	AMKSHSEKAHGH--GASRKETPQFFFSSPPPHSPL--SHGHIPSAIVLPNATHDYNTSFS	786
Qy	830	-----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLSSKSPN-----	865
Db	787	NSNAHKAEKKLQNIHPLTKSSKRDHRRSVDSRNTL--NDLLKHLNDPNSNPKAIMGDI	844
Qy	866	---HGVNLVENLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSY---GVDY	916
Db	845	QMAHQNLMLDPMGSMSEVPPKVPNREASILYSPPSTLPRNSPTKRVDPPTPGVPMTSLER	904
Qy	917	KRSYPTNSLTRSHQATTLKRNNTNSSNSSLRNQSFGRGD-NPPPAPQRVDSIQVHSSQ	975
Db	905	QRGYHKNSSQR-HSISAMPK-NLNSPNGVLLSRQPSMNRRGGYMPPTGAKVVDYIQ----	957
Qy	976	PSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDVPPKPSFAPLSTMKP	1025
Db	958	--GTPVSVHLQPSLSRQSSYTSGNTLPRTGLKRTPSLKPDVPPKPSFVPPQTPSVRP	1011

RESULT 11

Q8NFY6

ID Q8NFY6 PRELIMINARY; PRT; 998 AA.

AC 08NEY6;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Semaphorin 6D isoform 2.

GN SEMA6D.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Qu X., Zhai Y., Wei H., Yu Y., Tang F., He F.;
RT "Homo sapiens semaphorin 6D isoform 2 (SEMA6D.2) mRNA, complete cds.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF389427; AAM69450.1; -.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00630; Sema; 1.
SQ SEQUENCE 998 AA; 111730 MW; 3F46D6872E8D5344 CRC64;

Query Match 42.5%; Score 2315.5; DB 4; Length 998;
Best Local Similarity 45.8%; Pred. No. 1.3e-179;
Matches 493; Conservative 155; Mismatches 293; Indels 135; Gaps 26;

Qy 1 MRSEALLLYFTLL---HFAGAGFPEDSEPIISI SHGNYTKQYPVFVGHKPGRNTTQRHRLD 57
|| | | || ||| ||:: :|::||||| | :| | | :| ||||
Db 1 MRVFLLCAYILLLMVSQRAVSFPEDDEPLNTVDYHYSRQYPVFRG-RPSGNESQ-HRLD 58

Qy 58 IQMIMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGHKDEC 117
|::: : ||||| || :||::: |: :||||:||| | :| | |||||||
Db 59 FQLMLKIRDTLYIAGRQQVYTVNLNEMPKTEVIPNKKLTWRSRQQDRENCAMKGHKDEC 118

Qy 118 HNFIKVLLKKNDALFVCGTNAFPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALF 177
||||| : :||: :||||| ||| |::| ||| |:|||:|||:||: ||||||
Db 119 HNFIKVFPVRNDEMVFVCGTNAFPMCRYRLSTLEYDGEEISGLARCPFDARQTNVALF 178

Qy 178 ADGKLYSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFF 237
||||||| | ||| | |||||:|: | ||:|:|||:|||:|:|:||:|:|:|||
Db 179 ADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKEPHFLHAIETYGNVYFFF 238

Qy 238 EIAVEYNTMGKVVFPRAVQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQ 297
|||||:| :|| |: |||:|:||||| ||| | ||| ||| ||| ||| |||:|||
Db 239 EIAVEHNNLGKAVYSRVARIICKNDMGGSSQRVLEKHWTSFLKARLNCSVPGDSFYFDVLQ 298

Qy 298 AVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
::|:|:|:|| |: |:| | ||| |||:|:| ||| | ||| |||:||| ||| |||
Db 299 SITDIIQINGIPTVVGVTTLNSTITPGSAVCAFSMDDIEKVFKGRFKEQKTPDSVWTAVP 358

Qy 358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
:::||||| ||| | | || :|||:||:|||:||| | ||| | :| ||| :| |||
Db 359 EDKVPKPRPGCCAHKGLAEAYKTSIDFPDETLSFIKSHPLMSAVPPIADEPWFTKTRVR 418

Qy 418 YRLTKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGF-LNDSLFLLEMSVYNSEK 476
|||| |:| :||| |||:|||:||| |::| | |: | | |||:| |||:| |||
Db 419 YRLTAISVVDHSAGPYQNYTIVIFVGSEAGMVLKVLAK--TSPFSLNDSVLLEEIEAYNHAK 476

Qy 477 CSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKKTCIASRDPYCGWI 536
|| : | ||:|: :|||: | :|||:||:||| | |||:| |||:| |||:||| |||:
Db 477 CSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERYGSCKKSCIASRDPYCGWL 536

Qy 537 KEGGACSHLSPNSRLT-FEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQE 595

Db	537	SQ-GSCGRVTPGMLAEGYEQDTEFGNTAHLGDCHG-----	570
Qy	596	GYESRGGMILDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLGHDQLVPVTLLIAIV	655
Db	571	-----VRWE--VQSGES-----	593
Qy	656	IILAFVMGAVFSGITVYCVCD-HRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFG---	710
Db	594	FAAFVLGAFIAGVAVYCYRDMFVRKNRKI--HKDAESAQSCTDSSGSFAKLNGLFDSPVK	651
Qy	711	DTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKP	770
Db	652	EYQQNIDSPKLYSNLLTSRKELPPNGDTKSMVMDHRGQPPELAALPTPESTPVLHQKTLQ	711
Qy	771	SRGSREWERQNQLINACTKDMPPMGSPVIPTDLPLRASPISHPSVSVLPITQQGYQHEY-	829
Db	712	AMKSHSEKAHGH--GASRKETPQFFPSSPPPHSPL--SHGHIPSAIVLPNATHDYNTSFS	767
Qy	830	-----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLSSKSPN-----	865
Db	768	NSNAHKAEKKLQNIHPLTKSSKRDHRRSVDSRNTL--NDLLKHLNDPNSNPKAIMGDI	825
Qy	866	---HGVNLVENLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEMHHSSY---GVDY	916
Db	826	QMAHQNLMLDPGMSMEVPPKVPNREASLYSPPSTLPRNSPTKRVDPPTPGVPMTSLER	885
Qy	917	KRSYPTNSLTRSHQATTLKRNNTNSSNSSLRSRNQSFGRGD-NPPPAPQRVDSIQVHSSQ	975
Db	886	QRGYHKNSSQR-HSISAMPK-NLNSPNGVLLSRQPSMNRGGYMPTPTGAKVDYIQ----	938
Qy	976	PSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDVPPKPSFAPLSTMKP	1025
Db	939	--GTPVSVHLQPSLRSQSSYTSGTLPRTGLKRTPSLKPDVPPKPSFVPQTPSVRP	992

RESULT 12

Q8NFY3

ID Q8NFY3 PRELIMINARY; PRT; 1011 AA.
AC Q8NFY3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Semaphorin 6D isoform 1.
GN SEMA6D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Qu X., Wei H., Zhai Y., Yu Y., Tang F., He F.;
RT "Homo sapiens semaphorin 6D isoform 1 (SEMA6D.1) mRNA, complete cds."
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF389430; AAM69453.1; -.
DR InterPro; IPR001627; Sema.

Db	652	FAKLNGLFDSPVKEYQQNIDSPKLYSNLLTSRKELPPNGDTKSMVMDHRGQPPELAALPT	711
Qy	758	PESTPTIQQKRKPSRGSREWERNQNLINACTKDMPPMGSPIPTDLPLRASPISHIPSVVV	817
Db	712	PESTPVHLHQKTLQAMKSHSEKAHGH--GASRKETPQFFPSSPPHSPL--SHGHIPSAIL	767
Qy	818	LPITQQGYQHEY-----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLS	860
Db	768	LPNATHDYNTSFSNSNAHKAEKKLQNIDHPLTKSSSKRDHRRSVDSRNTL--NDLLKHLN	825
Qy	861	SKSPN-----HGVNLVENLDSL---PPKVPQREASLGPPGASLSQTGLSKRLEM	906
Db	826	DPNSNPKAIMGDIQMAHQNLMLDPGMGSMSEVPPKVPNREASLYSPPSTLPRNSPTKRVDV	885
Qy	907	HHSSSY---GVDYKRSPYPTNSLTRSHQATTLKRNNTNSSNSHLSRNQSFRGRD-NPPPA	962
Db	886	PTTPGVPMTSLERQRGYHKNSSQR-HSISAMPK-NLNSPNGVLLSRQPSMNRGGYMPPT	943
Qy	963	PQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDVPPKPSF	1016
Db	944	GAKVDYIQ-----GTPVSVHLQPSLSRQSSYTSNGTLPRTGLKRTPSLKPDVPPKPSF	996
Qy	1017	APLSTSMKP 1025	
Db	997	VPQTPSVP 1005	

RESULT 13

Q9P249

ID Q9P249 PRELIMINARY; PRT; 1022 AA.
AC Q9P249;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein KIAA1479 (Fragment).
GN KIAA1479.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human
RT genes.XVII.The complete sequences of 100 new cDNA clones from brain
RT which code for large proteins in vitro.";
RL DNA Res. 7:143-150(2000).
DR EMBL; AB040912; BAA96003.2; -.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
KW Hypothetical protein.

Db 663 FAKLNGLFDSPVKEYQQNIDSPKLYSNLLTSRKELEPPNGDTKSMVMDHRGQPPELAALPT 722
 Qy 758 PESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPIPTDPLRASPISHIPSVVV 817
 ||||| | || : | : : : | | : | | | | | || | || || : |
 Db 723 PESTPVLHQKTLQAMKSHSEKAHGH--GASRKETPQFFPSSPPPHSPL--SHGHIPSAIV 778
 Qy 818 LPITQQGYQHEY-----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLS 860
 || | : : | : | : | | : | || : : || : | : || : |
 Db 779 LPNATHDYNTSFSNSNAHKAEKKLQNIDHPLTKSSSKRDHRRSVDSRNTL--NDLLKHLN 836
 Qy 861 SKSPN-----HGVNLVENLDSL---PPKVPQREASLGPGASLSQTGLSKRLEM 906
 : | | : : | : | : | : | : | : | : | : | : | : | : |
 Db 837 DPNSNPKAIMGDIQMAHQNLMDPMGSMSEVPPKVPNREASLYSPPSTLPRNSPTKRVDV 896
 Qy 907 HHSSSY---GVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLSRNQSFGRGD-NPPPA 962
 : : : : | | || | | : : | | | | || | | || | | | |
 Db 897 PTTPGVPMTSLERQRGYHKNSSQR-HSISAMPK-NLNSPNGVLLSRQPSMNRRGGYMPTPT 954
 Qy 963 PQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDVPPKPSF 1016
 : || | | : | | : | : | : | : | : | : | : | : | : | : |
 Db 955 GAKVDYIQ-----GTPVSVHLQPSLSRQSSYTSNGTLPRTGLKRTPSLKPDVPPKPSF 1007
 Qy 1017 APLSTSMKP 1025
 | : | : |
 Db 1008 VPQTPSVRP 1016

RESULT 14

Q80TDO
 ID Q80TDO PRELIMINARY; PRT; 1009 AA.
 AC Q80TDO;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MKIAA1479 protein (Fragment).
 GN MKIAA1479.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22579291; PubMed=12693553;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
 RA Nakajima D., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
 RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:35-48(2003).
 DR EMBL; AK122515; BAC65797.1; -.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00630; Sema; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 1009 AA; 112808 MW; 7509F0B67332316B CRC64;

Qy	769	KPSRGSRREWERNQNLLINACTKDMPPMGSPVIPTDLPLRASP SHIPS VVVLPI TQQGYQH E	828
	:	: : : :	
Db	721	LQAMKSHSEKAHSH--GASRKEHPQFFPSSPPP HSPL --SHGHIPSAIVLPNATHDYNTS	776
Qy	829	Y-----VDQP---KMSEVAQMALEDQAATLEYKTIKEHLSS KSPN -----	865
	:	: : : : : : :	
Db	777	FSNSNAHKAEKKLQSMDHPLTKSSSKREHRRSVDSRNTL--NDLLKHLNDPNSNP KAILG	834
Qy	866	--HGVNLVENLD-----SLPPKVPQREASLGPPGASLSQTGLSKRLEMHSSSY---GV	914
	:	: : : : : :: : :	
Db	835	EIHMAHQTLMLDPVGPM AEVPPKVPN REALSYSPPSLPRNSPTKRV DVT PTPGVPMTSL	894
Qy	915	DYKR SYPTNSL TRSHQATT LKRNNNT NSNSHLSRNQS FGRGD -NPPPAPQRV VD SIQVHS	973
	:	: : : :	
Db	895	ERQR GYHKN SSQR-HSISAVPK- NLNSPN GVL LRSQPSMN RGGYMPTPTGA KVDYI Q--	949
Qy	974	SQPSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSL KPDV PPKPSFAPLSTSMKP	1025
		: : : : : : :	
Db	950	---GTPVSVHLOPSL SROSSYTSNGT LPRTGLKRTPSL KPDV PPKPSFV POTT SVRP	1003

RESULT 15

Q96JU9

ID Q96JU9 PRELIMINARY; PRT; 418 AA.
AC Q96JU9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ14961.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK027867; BAB55418.1; -.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00630; Sema; 1.
KW Hypothetical protein.
SQ SEQUENCE 418 AA; 47415 MW; 2E49A3F6C0564307 CRC64;

Query Match 40.6%; Score 2213; DB 4; Length 418;
 Best Local Similarity 100.0%; Pred. No. 7.3e-172;
 Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 MIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRADVDTCRMKGKHDECHNFI 121
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSQRADVDTCRMKGKHDECHNFI 60

Qy 122 KVLLKKNDDALFVCGTNAFPSCRNYKMDTLEPFGDEFSGMARCPTYDAKHANVALFADGK 181
|||
Db 61 KVLLKKNDDALFVCGTNAFPSCRNYKMDTLEPFGDEFSGMARCPTYDAKHANVALFADGK 120

Qy 182 LYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAV 241
|||
Db 121 LYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAV 180

Qy 242 EYNTMGKVVFPRAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTD 301
|||
Db 181 EYNTMGKVVFPRAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTD 240

Qy 302 VIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERV 361
|||
Db 241 VIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERV 300

Qy 362 PKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLT 421
|||
Db 301 PKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLT 360

Qy 422 KIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLLEEMSVYNSEK 476
|||
Db 361 KIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLLEEMSVYNSEK 415

Search completed: March 24, 2004, 13:16:25

Job time : 75.9691 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 13:07:38 ; Search time 20.5626 Seconds
(without alignments)
2608.241 Million cell updates/sec

Title: US-09-856-681A-2

Perfect score: 5450

Sequence: 1 MRSEALLYFTLLHFAGAGF.....PPKPSFAPLSTSMKPNDACT 1030

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	5450	100.0	1030	1	SM6A_HUMAN	Q9h2e6 homo sapien
2	4346.5	79.8	888	1	SM6A_MOUSE	O35464 mus musculu
3	2013.5	36.9	888	1	SM6B_HUMAN	Q9h3t3 homo sapien
4	1997	36.6	887	1	SM6B_RAT	O70141 rattus norv
5	1995	36.6	886	1	SM6B_MOUSE	O54951 mus musculu
6	1515.5	27.8	930	1	SM6C_HUMAN	Q9h3t2 homo sapien
7	1493.5	27.4	931	1	SM6C_MOUSE	Q9wtm3 mus musculu
8	1491	27.4	960	1	SM6C_RAT	Q9wtl3 rattus norv
9	971.5	17.8	730	1	SM1A_SCHAM	Q26473 schistocerc
10	932.5	17.1	771	1	SM1A_DROME	Q24322 drosophila
11	858	15.7	772	1	SM3A_RAT	Q63548 rattus norv
12	853	15.7	772	1	SM3A_MOUSE	O08665 mus musculu
13	852.5	15.6	771	1	SM3A_HUMAN	Q14563 homo sapien
14	845	15.5	712	1	SM1A_TRICF	Q26972 tribolium c
15	845	15.5	778	1	SZ1B_BRARE	Q9w686 brachydanio
16	845	15.5	860	1	SZ1A_BRARE	Q9w7j1 brachydanio
17	839.5	15.4	772	1	SM3A_CHICK	Q90607 gallus gall

18	830	15.2	1074	1	SM5A_HUMAN	Q13591 homo sapien
19	826	15.2	749	1	SM3B_HUMAN	Q13214 homo sapien
20	825.5	15.1	1077	1	SM5A_MOUSE	Q62217 mus musculu
21	803	14.7	748	1	SM3B_MOUSE	Q62177 mus musculu
22	803	14.7	764	1	SMZ2_BRARE	Q9w6g6 brachydanio
23	797	14.6	777	1	SM3D_HUMAN	O95025 homo sapien
24	793.5	14.6	761	1	SM3D_CHICK	Q90663 gallus gall
25	789	14.5	712	1	SM1A_CAEEL	Q17330 caenorhabdi
26	770.5	14.1	1093	1	SM5B_HUMAN	Q9p283 homo sapien
27	766	14.1	1093	1	SM5B_MOUSE	Q60519 mus musculu
28	762.5	14.0	706	1	SM2A_DROME	Q24323 drosophila
29	762	14.0	775	1	SM3E_HUMAN	O15041 homo sapien
30	752	13.8	751	1	SM3C_CHICK	O42236 gallus gall
31	751	13.8	861	1	SM4D_MOUSE	O09126 mus musculu
32	750.5	13.8	697	1	SM2A_SCHGR	Q9xzc8 schistocerc
33	749	13.7	785	1	SM3F_HUMAN	Q13275 homo sapien
34	744.5	13.7	785	1	SM3F_MOUSE	O88632 mus musculu
35	739	13.6	775	1	SM3E_MOUSE	P70275 mus musculu
36	737	13.5	751	1	SM3C_MOUSE	Q62181 mus musculu
37	735.5	13.5	862	1	SM4D_HUMAN	Q92854 homo sapien
38	733.5	13.5	785	1	SM3E_CHICK	O42237 gallus gall
39	733	13.4	751	1	SM3C_HUMAN	Q99985 homo sapien
40	700.5	12.9	766	1	SMZ7_BRARE	Q9yhx4 brachydanio
41	692	12.7	834	1	SM4C_MOUSE	Q64151 mus musculu
42	681	12.5	832	1	SM4B_HUMAN	Q9npr2 homo sapien
43	671	12.3	761	1	SM4A_HUMAN	Q9h3s1 homo sapien
44	664	12.2	776	1	SM4F_RAT	Q9z143 rattus norv
45	658	12.1	777	1	SM4F_MOUSE	Q9z123 mus musculu

ALIGNMENTS

RESULT 1

SM6A_HUMAN

ID SM6A_HUMAN STANDARD; PRT; 1030 AA.

AC Q9H2E6; Q9P2H9;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Semaphorin 6A precursor (Semaphorin VIA) (Sema VIA) (Semaphorin 6A-1)

DE (SEMA6A-1).

GN SEMA6A OR KIAA1368.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND INTERACTION WITH EVL.

RX MEDLINE=20564339; PubMed=10993894;

RA Klostermann A., Lutz B., Gertler F., Behl C.;

RT "The orthologous human and murine semaphorin 6A-1 proteins (SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-stimulated phosphoprotein-like protein (EVL) via a novel carboxyl-terminal zyxin-like domain.";

RL J. Biol. Chem. 275:39647-39653(2000).

RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20181126; PubMed=10718198;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:65-73(2000).
CC -!- FUNCTION: Can act as repulsive axon guidance cues. May play a role
CC in channeling sympathetic axons into the sympathetic chains and
CC controlling the temporal sequence of sympathetic target
CC innervation (By similarity).
CC -!- SUBUNIT: Active as a homodimer or oligomer. Interacts with EVL.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9H2E6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9H2E6-2; Sequence=VSP_007113;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -----
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CC -----
DR EMBL; AF279656; AAG29378.1; -.
DR EMBL; AB037789; BAA92606.1; ALT_INIT.
DR Genew; HGNC:10738; SEMA6A.
DR MIM; 605885; -.
DR GO; GO:0030424; C:axon; NAS.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0008580; F:cytoskeletal regulator activity; NAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006915; P:apoptosis; NAS.
DR GO; GO:0007411; P:axon guidance; NAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; NAS.
DR GO; GO:0007399; P:neurogenesis; NAS.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
KW Developmental protein; Alternative splicing.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1030 SEMAPHORIN 6A.
FT DOMAIN 19 649 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 650 670 POTENTIAL.
FT DOMAIN 671 1030 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 56 491 SEMA.

FT DOMAIN 792 819 PRO-RICH.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 576 576 N -> NDISTPLPDNEMSYNTVY (in isoform 2).
 FT /FTId=VSP_007113.
 SQ SEQUENCE 1030 AA; 114368 MW; A57B79C10AEC4B34 CRC64;

 Query Match 100.0%; Score 5450; DB 1; Length 1030;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
 |||||||
 Db 1 MRSEALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

 Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKLTWKSQADVDTCRMKGHKDECHNF 120
 |||||||
 Db 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEIYCSKLTWKSQADVDTCRMKGHKDECHNF 120

 Qy 121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCYDAKHANVALFADG 180
 |||||||
 Db 121 IKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCYDAKHANVALFADG 180

 Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240
 |||||||
 Db 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240

 Qy 241 VEYNTMGKVVFPRAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGSYFNLQAVT 300
 |||||||
 Db 241 VEYNTMGKVVFPRAQVCKNDMGGSRVLEKQWTSFLKARLNCSVPGSYFNLQAVT 300

 Qy 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
 |||||||
 Db 301 DVIRINGRDVVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360

 Qy 361 VPKRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
 |||||||
 Db 361 VPKRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420

 Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYD 480
 |||||||
 Db 421 TKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYD 480

 Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKTCIASRDPYCGWIKEGG 540
 |||||||
 Db 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKTCIASRDPYCGWIKEGG 540

 Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESR 600
 |||||||
 Db 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSDSTAQEYESR 600

 Qy 601 GGMLDWKHLLDSPDSTDPLGAVSSHNDKKGVIRESYLGHDQLVPVTLLAIAVILAFV 660
 |||||||

Db 601 GGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLQLVPVTLLIAVILAFV 660
 Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSVTLSGLFGDTQSKDPKPE 720
 |||||||
 Db 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSVTLSGLFGDTQSKDPKPE 720
 Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSRGSREWERN 780
 |||||||
 Db 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSRGSREWERN 780
 Qy 781 QNLINACTKDMPPMGSPVIPTDPLRASPISHPSVVVLPIQQGYQHEYVDQPKMSEVAQ 840
 |||||||
 Db 781 QNLINACTKDMPPMGSPVIPTDPLRASPISHPSVVVLPIQQGYQHEYVDQPKMSEVAQ 840
 Qy 841 MALEDQAATLEYKTIKEHLSSKSPNHGVLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
 |||||||
 Db 841 MALEDQAATLEYKTIKEHLSSKSPNHGVLVENLDSLPPKVPQREASLGPPGASLSQTGL 900
 Qy 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSHLSRNQSFGRGDNPP 960
 |||||||
 Db 901 SKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNNTNSSNSHLSRNQSFGRGDNPP 960
 Qy 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSILKPDVPPKPSFAPLS 1020
 |||||||
 Db 961 PAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSILKPDVPPKPSFAPLS 1020
 Qy 1021 TSMKPNDACT 1030
 |||||||
 Db 1021 TSMKPNDACT 1030

RESULT 2

SM6A_MOUSE
 ID SM6A_MOUSE STANDARD; PRT; 888 AA.
 AC O35464;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Semaphorin 6A precursor (Semaphorin VIA) (Sema VIA) (Semaphorin 6A-1)
 DE (SEMA6A-1) (Semaphorin Q) (Sema Q).
 GN SEMA6A OR SEMAQ.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97348468; PubMed=9204478;
 RA Zhou L., White F.A., Lentz S.I., Wright D.E., Fisher D.A.,
 RA Snider W.D.;
 RT "Cloning and expression of a novel murine semaphorin with structural
 RT similarity to insect semaphorin I.";
 RL Mol. Cell. Neurosci. 9:26-41(1997).
 RN [2]
 RP INTERACTION WITH EVL.
 RX MEDLINE=20564339; PubMed=10993894;
 RA Klostermann A., Lutz B., Gertler F., Behl C.;

RT "The orthologous human and murine semaphorin 6A-1 proteins
 RT (SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-stimulated
 RT phosphoprotein-like protein (EVL) via a novel carboxyl-terminal
 RT zyxin-like domain.";
 RL J. Biol. Chem. 275:39647-39653(2000).
 CC -!- FUNCTION: Can act as repulsive axon guidance cues. May play a role
 CC in channeling sympathetic axons into the sympathetic chains and
 CC controlling the temporal sequence of sympathetic target
 CC innervation.
 CC -!- SUBUNIT: Active as a homodimer or oligomer. Interacts with EVL.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Particularly high levels in spinal cord,
 CC cerebellum, metencephalon, superior and inferior colliculus,
 CC diencephalon, olfactory bulb and eye.
 CC -!- DEVELOPMENTAL STAGE: Temporally and spatially regulated during
 CC development.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; AF030430; AAB86408.1; -.
 DR MGD; MGI:1203727; Sema6a.
 DR GO; GO:0030424; C:axon; NAS.
 DR GO; GO:0016020; C:membrane; NAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0006915; P:apoptosis; NAS.
 DR GO; GO:0007411; P:axon guidance; NAS.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 888 SEMAPHORIN 6A.
 FT DOMAIN 19 649 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 650 670 POTENTIAL.
 FT DOMAIN 671 888 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 56 491 SEMA.
 FT DOMAIN 792 819 PRO-RICH.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 888 AA; 99075 MW; C7094FC2BB345C57 CRC64;

Query Match 79.8%; Score 4346.5; DB 1; Length 888;

Best Local Similarity 94.4%; Pred. No. 9.7e-273;
Matches 816; Conservative 24; Mismatches 23; Indels 1; Gaps 1;

Qy 1 MRSEALLLYFTLLLHFAGAGFPEDSEPISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60
|| |||| |||| ||||||||||||||||||||||||||||||||||||||
Db 1 MRPAALLLCLLHCAGAGFPEDSEPISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQM 60

Qy 61 IMIMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGHKDECHNF 120
||||| ||||:||||||||||||||||||||||||||||||||||||
Db 61 IMIMNRTLYVAARDHIYTVDIDTSHTEEYCSKKLTWKSQADVDTCRMKGHKDECHNF 120

Qy 121 IKVLLKKNDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPTYDAKHANVALFADG 180
||||||| ||||| ||||||| :||||| ||||||| :||||| ||||||| :|||||
Db 121 IKVLLKKNDALFVCGTNAFNPSCRNYRVDTLETFGDEFSGMARCPTYDAKHANIALFADG 180

Qy 181 KLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240
||||||| ||||| :||||| ||||||| ||||||| ||||||| |||||||
Db 181 KLYSATVTDFLAIDAVIYRSLGDSPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIA 240

Qy 241 VEYNTMGKVVPRVAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300
||||||| ||||| ||||| ||||| :||||| ||||||| |||||||
Db 241 VEYNTMGKVVPRVAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVT 300

Qy 301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
||||||| ||||| ||||| :||||| ||||||| :||||| |||||||
Db 301 DVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLDIANVFTGRFKEQKSPDSTWTPVPDER 360

Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
||||||| ||||| :||||| ||||||| ||||||| |||||||
Db 361 VPKPRPGCCAGSSSLEYATSNEFPDDTLNFIKTHPLMDEAVPSIINRPWFLRTMVRYRL 420

Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYD 480
||||| ||||||| ||||||| :||||| ||||||| :||| |||||||
Db 421 TKIAVDNAAGPYQNHTVVFLGSEKGIIILKFLARIGSSGFLNGSLFLLEEMNVYNPEKCSYD 480

Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKKTCIASRDPYCGWIKEGG 540
||||||| ||||| ||||||| :||||| ||||||| :|||
Db 481 GVEDKRIMGMQLDRASGLYVAFSTCVIKVPLGRcerHGKCKKTCIASRDPYCGWVRESG 540

Qy 541 ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTSYSTAQEGYESR 600
:||| ||||||| ||||||| :||||| :||| ||||||| ::|||
Db 541 SCAHLSPLSRLTFEQDIERGNTDGLGDCHNSFVALNGHASSLYPSTTSASRDGYESR 600

Qy 601 GGMLDWKHLLDSPSTDPLGAVSSHNDQDKGVIRESYLKGDQLVPVTLLAIAVILAFV 660
||||| ||:::| ||||||| :||||| ||||||| :|||||
Db 601 GGMLDWNDLLEAPGSTDPLGAVSSHNDQDKGVIRESYLKSNDQLVPVTLLAIAVILAFV 660

Qy 661 MGAVFSGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGLFGDTQSKDPKPE 720
||||||| ||||||| ||||||| :||||| |||||||
Db 661 MGAVFSGIIVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTLSGLFGDTQSKDPKPE 720

Qy 721 AILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGREWERN 780
||||||| ||||||| :||||| ||||||| :||||| :|||||
Db 721 AILTPLMHNGKLATPSNTAKMLIKADQHHLDLTALPTPESTPTLQEKRKPNRGREWERN 780

Qy 781 QNLINACTKDMPPMGSPIPTDLPLRASPISHPSVVLPITQQGYQHEYVDQPKMSE-VA 839
||:||||| ||||||| ||||||| ||||||| ||||||| ||

Db 781 QNIINACTKDMPPMGSPVIPTDLPLRASPShIPSVVLPITQQGYQHEYVDQPKMSEVVA 840
Qy 840 QMALEDQAATLEYKTIKEHLSSKS 863
||| :|
Db 841 QMALEDQAATLEYKTIKEHLSSES 864

RESULT 3
SM6B_HUMAN
ID SM6B_HUMAN STANDARD; PRT; 888 AA.
AC Q9H3T3; Q9NRK9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Semaphorin 6B precursor (Semaphorin Z) (Sema Z).
GN SEMA6B OR SEMAZ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA Kimura T., Ishida H.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=21248680; PubMed=11350127;
RA Correa R.G., Sasahara R.M., Bengtson M.H., Katayama M.L.H.,
RA Salim A.C.M., Brentani M.M., Sogayar M.C., de Souza S.J.,
RA Simpson A.J.G.;
RT "Human semaphorin 6b.";
RL Genomics 73:343-348(2001).
CC -!- FUNCTION: MAY PLAY A ROLE IN BOTH PERIPHERAL AND CENTRAL NERVOUS
CC SYSTEM DEVELOPMENT (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=Q9H3T3-1; Sequence=Displayed;
CC Name=2; Synonyms=6B.1;
CC IsoId=Q9H3T3-2; Sequence=VSP_006044, VSP_006045;
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -----
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CC -----
DR EMBL; AB022433; BAB20669.1; -.
DR EMBL; AF216389; AAF87661.1; -.
DR Genew; HGNC:10739; SEMA6B.

DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 888 SEMAPHORIN 6B.
 FT DOMAIN 26 603 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 604 624 POTENTIAL.
 FT DOMAIN 625 888 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 238 547 SEMA.
 FT DOMAIN 661 674 POLY-GLY.
 FT DOMAIN 750 753 POLY-LEU.
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 471 517 LSVFLEEFETYRPDRCGRPGGGGETQQLLSLEDAASGGLL
 AAFPRC -> RVCQVGHACRVCVHERRSWWPQRPGRLSRR
 WGFQKARGPPRTRLGV (in isoform 2).
 FT /FTId=VSP_006044.
 FT VARSPLIC 518 888 Missing (in isoform 2).
 FT /FTId=VSP_006045.
 FT CONFLICT 30 30 D -> E (IN REF. 2).
 SQ SEQUENCE 888 AA; 95270 MW; 6FFB44D6828C70CB CRC64;

Query Match 36.9%; Score 2013.5; DB 1; Length 888;
 Best Local Similarity 45.3%; Pred. No. 3.6e-122;
 Matches 424; Conservative 129; Mismatches 241; Indels 141; Gaps 20;

Qy	5 ALLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQR--HRLDIQMIM 62 ::: : :: ::
Db	12 ALLLLLLLGGAHGLFPEDPPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGADDLNIQRVL 71
Qy	63 IMNGTLYIAARDHIYTVDIDTSHTEEYCSKKLTWKSQRADVDTCRMKGHKDECHNFIK 122 : :: :: ::: : : : : : :: : ::
Db	72 RVNRTLFIGDRDNLYRVELEPPSTELRYQRKLTWRSNPSDINVCRMKGKQEGERNFVK 131
Qy	123 VLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDFSGMARCPYDAKHANVALFADGKL 182 :: : : : :
Db	132 VLLLRDESTLFVCGSNAFNPCANYSIDLQPVGDNISMARCPYDPKHNVALFSDGML 191
Qy	183 YSATVTDFAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREIAVE 242 :: : : :: : :
Db	192 FTATVTDFAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWSHVYFFFREIAVE 251
Qy	243 YNTMGKVVFPRAQVCKNDMGGSQLQWTSFLKARLNCSVPGDSHFYFNILQAVTDV 302 : : : : :
Db	252 FNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTGV 311
Qy	303 IRINGRDVVLATFSTPYNSIPGSACAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVP 362 : : : : : : :

Db 312 VSLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAASFEGRFREQKSPEIWTVPEDQVP 371
 Qy 363 KPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTK 422
 :||||||| :| |: ||| ||:|||||||||: :|| ||::|::||:
 Db 372 RPRPGCCAAPGM--QYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLHQLTR 429
 Qy 423 IAVDTAAGPYQNHTVVFLGSEKGIIILKFLAR--IGNSGFLNDSLLEEMSVYNSEKCSYD 480
 :||| ||: | ||||||| | :||| | || |:||| | ::|
 Db 430 VAVDVGAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVLEEFETYRPDRCGRP 489
 Qy 481 GVED--KRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKTCIASRDPYCGWIKE 538
 | : :|:: :|| | | || ||::||: ||::: |:||| | :||| :
 Db 490 GGGETGQRLLSLEDAASGGLLAAFPVCVVRPVARCQQYSGCMKNCIGSQDPYCGWAPD 549
 Qy 539 GGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQEY 598
 |:| ||| :| ||||: :| |||||
 Db 550 -GSCIFLSPGPTRAFAEQDVSGASTSGLGDC----- 578
 Qy 599 SRGGMLDWKHLLSPDSTDPLGAVSSHNHQDKKGVIRESYLNKGHDQLVPVTLLIAVILA 658
 |::| | : ||| || : :|
 Db 579 -----TGLLRASLSEDRAGLVSVNLLVTSSVAA 606
 Qy 659 FVMGAVFSGITV-YCVCDFHRRKDVAVQRKEKE--LTHSRRGSMSSVTKLSGLFGDTQSK 715
 ||:||| || :| :| |:::| :||:|| | | ::||:| | : :::
 Db 607 FVVGAVVSGFSVGWFVGLRERELA--RRKDKEAI LAHGAGEAVLSVRL---GERRAQ 660
 Qy 716 DP-----KPEAILTPLMHNGKLATPGNTAK-MLIKADQHHLSDLTALPTPEST 761
 | |::| ||| || | | |::| | ||| | | :|
 Db 661 GPGGRGGGGGGGAGVPPEALLAPLMQNG-----WAKATLLQGGPHDLDGGLPTPEQT 713
 Qy 762 PTLQQKRKP-----SRGSREWERNQNLINACTKDMPPMGSPVIPTDLP---LRASPSH 811
 | | ||| | :| | |: | |::| | :|
 Db 714 P-LPKQLPPTPHPHHALGPRAWDH-----GHPLLPAASSLLLLAPAR 757
 Qy 812 IPSVVVLPIQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGVNLV 871
 | | | | :| : | | |: : : :| ::
 Db 758 APEQPPAPGEPTPDGRILYAARPGRASHGDFPLTPHASPDRRVV----SAPTGPLDPA 811
 Qy 872 ENLDSLP-PKVPQREASL-----GPPGASLSQT 898
 | | | | | | | | :| :| :|
 Db 812 SAADGLPRPWSPPPPTGSLRRPLGPHAPPAATLRR 846

RESULT 4

SM6B_RAT

ID SM6B_RAT STANDARD; PRT; 887 AA.
 AC 070141;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Semaphorin 6B precursor (Semaphorin Z) (Sema Z).
 GN SEMA6B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=98087397; PubMed=9427525;
RA Kikuchi K., Ishida H., Kimura T.;
RT "Molecular cloning of a novel member of semaphorin family genes,
semaphorin Z.";
RL Brain Res. Mol. Brain Res. 51:229-237(1997).
CC -!- FUNCTION: MAY PLAY A ROLE IN BOTH PERIPHERAL AND CENTRAL NERVOUS
CC SYSTEM DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DEVELOPMENTAL STAGE: DETECTED IN THE FIRST BRANCHIAL ARCH OF
CC EMBRYONIC DAY 11 (E11) EMBRYO, AND SUBSEQUENTLY IN THE MYOTOMES
CC AND THE DORSAL ROOT GANGLIA IN DEVELOPING SOMITES FROM E11.5
CC THROUGH E13.5, BUT NOT IN THE BRAIN. HOWEVER, AT E15, 18, 21 AND
CC P0, SEMAZ WAS HIGHLY EXPRESSED IN THE BRAIN.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB000776; BAA25687.1; -.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
KW Developmental protein.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 887 SEMAPHORIN 6B.
FT DOMAIN 27 605 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 606 626 POTENTIAL.
FT DOMAIN 627 887 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 239 549 SEMA.
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 887 AA; 95752 MW; 09543F3F202CD301 CRC64;

Query Match 36.6%; Score 1997; DB 1; Length 887;
Best Local Similarity 42.7%; Pred. No. 4.2e-121;
Matches 433; Conservative 132; Mismatches 260; Indels 190; Gaps 25;

Qy 2 RSEALLLYFTLLHFAGAGFPEDSEPISHGNYTKQYPVFGHKPGRNTTQR--HRLDIQ 59
| || || ||:: ||:: :|| |||| | || | ||:||
Db 10 RPALLFLLLLLRLVTHGLFPDEPPPLSVAPRDYLSHYPVFGSGPGRLTAEAGAEDLNIQ 69

Qy 60 MIMIMNGTLYIAARDHIYTVIDTSHTEIYCSKKLTWKSQRQADVDTCRMKGHKDECHN 119
:: :| ||:| ||::| |::: | : |: :|||:| :|:| ||||| :|||
Db 70 RVLRVNRTLFIGDRDNLYQVELEPSTSTELRYQRKLTWRSNPSIDVCRMKGKQEGERN 129

Qy 120 FIKVLLKKNDDALFVCGTNAFNPSCKNYKMDTLEPGDEFSGMARCPTYDAKHANVALFAD 179
|:|||| ::: |||||:||| | ||| |||: || ||||||| |||||||:
Db 130 FVKVLLLRDESTLFVCGSNAFNPICANYSMDTLQLLGDNISGMARCPYDPKHANVALFSD 189

Qy 180 GKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDIYFFFREI 239
| |::| ||||||| |||||: ||| ||| ||| ||| |||:| :| |||:
Db 190 GMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREI 249

Qy 240 AVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAV 299
|:|:| :| | | |:| | | | | | | | | | | | | | | | | |:
Db 250 AMEFNYLEKVVVSRAVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAV 309

Qy 300 TDVIRINGRDVVLATFSTPYNSIPGSACVACYDMLDIASVFTGRFKEQKSPDSTWTPVPDE 359
. | : | | | | | | | | | | | | | | | | | | | | | |:
Db 310 TGVVSLGGRPVILAVFSTPSNSIPGSACAFDMNQVAVFEGRFREQKSPESIWTPVPED 369

Qy 360 RVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYR 419
:|:| | | | | | | | | | | | | | | | | | | | | | |:
Db 370 QVPRPRPGCCAAPGM--QYNASNALPDEILNFVKTHPLMDEAVPSLGHSPWIVRTLIRHQ 427

Qy 420 LTKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLAR--IGNSGFLNDSLFLLEEMSVYNSEKC 477
| |:| | | | | | | | | | | | | | | | | | | | | |:
Db 428 LTRVAVDVGAGPWGNQTIVFLGSEVGTVLKFLVKPNASVSGTTGPSIFLEEFETYRPDRC 487

Qy 478 ---SYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCEHGCKKTCIASRDPYCG 534
| | | :|:| :| | | | | | | | | | | | | | | | | |:
Db 488 GRSSSAGEWGQRLLSLELDAASGGLAAFPRCVVVPVARCQLYSGCMKNICIGSQDPYCG 547

Qy 535 WIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSLLPSTTSSTAQ 594
| : |:| | | | | | | | | | | | | | | | | | | | |:
Db 548 WAPD-GSCI FLRPGTSATFEQDVSGASTSGLGDC----- 580

Qy 595 EGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGDQLVPVTLLAIA 654
| :| | | | | | | | | | | | | | | | | | | | | |:
Db 581 -----TGLLRASLSDDRAGLVSVNLLVTS 604

Qy 655 VILAFVMGAVFSGITV-YCVCDHRRKDVAVVQRKEKE--LTHSRRGSMSSVTKL----- 705
| | |:| | | | | | | | | | | | | | | | | | | |:
Db 605 SVAAFVVGAVVSGFSVGFWVGLRERREL--RRKDKEAILAHGGSEAVLSVSRLGERRGT 662

Qy 706 --SGLFGDTQS KDPKPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPT 763
| | | | | | | | | | | | | | | | | | | | | | | | |:
Db 663 GTGGRRGGAGGGPGGPPEALLAPLMQNGW-----TKAALLHGGPHDLDGGLPTPEQTP- 715

Qy 764 LQQKRKPSR-----GSREWERNQNLI NACTK-----DMPPMGS PVIPTD-- 802
| | | | | | | | | | | | | | | | | | | | | | | | |:
Db 716 LPQKRLPTTHPHAHALGPRAWDHSHALLSASASTSLLLHTRAPEQPP----VPTESG 770

Qy 803 -----LPLRASP SHIPS VVLPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK 856
| | | | | | | | | | | | | | | | | | | | | | | | |:
Db 771 PESRLCAPRSCRASHPGDFPLTP-----HASPDRRRVVSAPTGPLDSSSVG----- 816

Qy 857 EHLSSKSPN HGVNLLVENLDSL P-KVVPQREASL-----GPPGASLSQTGLSKRLEMHS 909

| | | | | :|| | | | :| :| | :|
Db 817 -----DDLPGPWSPPATSSLRPGPHGPTAALRRT-----HT 849
Qy 910 SSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSHLSRNQSFGRGD-NPPPAP 963
: | : | | | :| :| | | : | | |
Db 850 FNSG----EARPGGHRPRRHA-----PADSTHL---LPCGTGERTAPPVP 887

RESULT 5

SM6B_MOUSE

ID SM6B_MOUSE STANDARD; PRT; 886 AA.
AC O54951;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Semaphorin 6B precursor (Semaphorin VIB) (Sema VIB) (Semaphorin N)
DE (Sema N).
GN SEMA6B OR SEMAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98027184; PubMed=9361278;
RA Eckhardt F., Behar O., Calautti E., Yonezawa K., Nishimoto I.,
RA Fishman M.C.;
RT "A novel transmembrane semaphorin can bind c-src.";
RL Mol. Cell. Neurosci. 9:409-419(1997).
CC -!- SUBUNIT: HOMODIMER. BINDS SPECIFICALLY THE SH3 DOMAIN OF THE
CC PROTOONCOGENE C-SRC.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: During development it is expressed in
CC subregions of the nervous system and is particularly prominent in
CC muscle. In adulthood, it is expressed ubiquitously.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -----
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CC -----
DR EMBL; AF036585; AAC00493.1; -.
DR MGD; MGI:1202889; Sema6b.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
KW Developmental protein.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 886 SEMAPHORIN 6B.

Qy 598 ESRGGMLDWKHLLEDSPSTDPLGAVSSHNHQDKKGVIRESYLGHDQLVPVTLLAIAVIL 657
 |::| | ||| || : :
 Db 581 -----TGLLRASLSDDRAGLVSVNLLVTSSVA 607

 Qy 658 AFVMGAVFSGITV-YCVCDHRRKDVAVQRKEKE--LTHSRRGSMSSVTKLSGLFGDTQS 714
 ||||:|||| || :| :| |:::| :||:|| | | ::|:| :| :|:
 Db 608 AFVVGAVVSGFSVGFWFVGLRERELA--RRKDKEAILAHGGSEAVLSVSRL---GERRG 661

 Qy 715 KDP-----KPEAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTP 762
 | |||:| ||| || | | :| :| ||| ||| |||:
 Db 662 TGPGRGGAGGGPGGPPEALLAPLMQNGW-----TKAALLHGGPHDLDTGLLPTPEQTP 715

 Qy 763 TLQQKRKP-----SRGSREWERNQNLINACTKDMPPMGSPVIPTDL---PLRASPSh 811
 | ||| | :| ||| |:| :| ||| | | | :| :|:
 Db 716 -LPQKRLPTPHAHALGSRAWDHSHALLSASAS-----TSLLLLAPARASEQ- 762

 Qy 812 IPSVVVLPIQQGYQHEYVDQP---KMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHGV 868
 | | | | :| :| | :| | | | | :| :| :|:
 Db 763 -PQVPAEPGPE----SRLCAPRSCRASHPGDFPLTPHASPDRRRVVSAPTGPLDPSVG- 815

 Qy 869 NLVENLDSLP-PKVPQREASL-----GPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYP 921
 | ||| | | :| | ||| |:| :| |:| :| :|:
 Db 816 -----DGLPGPWSPPATSSLRRPGPHGPPTAALRRT-----HTFNSG---EARP 856

 Qy 922 TNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGD-NPPPAP 963
 | | :|:| | | | :| | | |:
 Db 857 GGHRPRRHP-----PADSTHL---LPCGTGERTAPPV 886

RESULT 6

SM6C_HUMAN

ID SM6C_HUMAN STANDARD; PRT; 930 AA.
 AC Q9H3T2; Q8WXT8; Q8WXT9; Q8WXU0; Q96JF8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 6C precursor (Semaphorin Y) (Sema Y).
 GN SEMA6C OR SEMAY OR KIAA1869.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RA Kimura T., Ishida H.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Brain;
 RA Qu X., Zhai Y., Wei H., Zhang C., Xing G., Yu Y., Wu S., Zhang Y.,
 RA Ouyang S., Zhou G., He F.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=21245130; PubMed=11347906;

RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XX.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 8:85-95(2001).
 CC -!- FUNCTION: May be a stop signal for the dorsal root ganglion
 CC neurons in their target areas, and possibly also for other
 CC neurons. May also be involved in the maintenance and remodeling of
 CC neuronal connections (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=Short 1;
 CC IsoId=Q9H3T2-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short 2;
 CC IsoId=Q9H3T2-2; Sequence=VSP_006046, VSP_006047;
 CC Name=3; Synonyms=Long;
 CC IsoId=Q9H3T2-3; Sequence=VSP_006047;
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; AB022434; BAB20670.1; -.
 DR EMBL; AF339152; AAL72098.1; -.
 DR EMBL; AF339153; AAL72099.1; -.
 DR EMBL; AF339154; AAL72100.1; -.
 DR EMBL; AB058772; BAB47498.1; ALT_INIT.
 DR Genew; HGNC:10740; SEMA6C.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
 KW Developmental protein; Alternative splicing.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 930 SEMAPHORIN 6C.
 FT DOMAIN 25 604 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 605 625 POTENTIAL.
 FT DOMAIN 626 930 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 233 540 SEMA.
 FT DOMAIN 662 667 POLY-PRO.
 FT DOMAIN 752 755 POLY-PRO.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 184 223 Missing (in isoform 2).
 FT VARSPLIC 586 586 /FTId=VSP_006046.
 FT VARSPLIC 586 586 Y -> YVLPGPGPSPGTSPSPSDAHPRPQSSTLGVHTR
 FT VARSPLIC 586 586 (in isoform 2 and isoform 3).

Qy 709 FGDTQSKDPKP--EAILTPLMHNGKLATPGNTAKMLIKADQHHLTLALPTPESTPTLQQ 766
 | : | :| || :: | | | :| |||||||| |
 Db 660 -GGPEPPPPSKDGDAVQTPQLYTTFLPPEGVPPP-----ELACLPTPESTPELPV 709

 Qy 767 KRKPSRGSREWERNQNLINACTKDMPPMGSPIPTDLPLRASPSh----IPSVVVLPIt 821
 | : | || || | | : | | : | | : | |
 Db 710 KHLRAAGD-PWEWNQNQRNNA-----KEGPGRSRGGHAAGGPAPRVLVRP-- 752

 Qy 822 QQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHL---SSKSPNHGVNLVENLDS- 876
 | | : | | | | : | | : | | | | | | | |
 Db 753 -----PPPGCPGQ-----AVEVTITLELLRYLHGPQPPrKGAEPPAPLTSR 793

 Qy 877 -LPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLK 935
 |||: | | | | : | | | : | | | | | | | |
 Db 794 ALPPE--PAPALLGGPSPRPHECASPLRLDV-----PPEGRCASAPA--- 833

 Qy 936 RNNTNSSNSHl---SRNQSFGRGDNPpPAPQRVDSIQVHSSQPSGQAVTVSRQPS--- 988
 | : | | | | | | | | | | | | | | | | | |
 Db 834 -RPALSAPAPRLGVGGGRRLPFSGHRAPPAALLTRV-----PSGGPSRYSGGPGKHL 883

 Qy 989 --LNAYNSLTRSGLKRTPSLKPDVPPKPSF-APLSTSMKPN 1026
 | | | | | | : | | | | | | | | | | | | |
 Db 884 LYLRPEGYRGRALKRVDVEKPQLSLKPPLVGPSRQAVPN 924

RESULT 7

SM6C_MOUSE

ID SM6C_MOUSE STANDARD; PRT; 931 AA.
 AC Q9WTM3;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Semaphorin 6C precursor (Semaphorin Y) (Sema Y).
 GN SEMA6C OR SEMAY.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=99160821; PubMed=10049528;
 RA Kikuchi K., Chedotal A., Hanafusa H., Ujimasa Y., de Castro F.,
 RA Goodman C.S., Kimura T.;
 RT "Cloning and characterization of a novel class VI semaphorin,
 RT semaphorin Y.";
 RL Mol. Cell. Neurosci. 13:9-23(1999).
 CC --!- FUNCTION: May be a stop signal for the dorsal root ganglion
 CC neurons in their target areas, and possibly also for other
 CC neurons. May also be involved in the maintenance and remodeling of
 CC neuronal connections (By similarity).
 CC --!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC --!- SIMILARITY: Belongs to the semaphorin family.
 CC --!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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CC-----
DR EMBL; AB013729; BAA76294.1; -.
DR MGD; MGI:1338032; Sema6c.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00630; Sema; 1.
KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
KW Developmental protein.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 931 SEMAPHORIN 6C.
FT DOMAIN 26 605 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 606 626 POTENTIAL.
FT DOMAIN 627 931 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 234 541 SEMA.
FT DOMAIN 663 669 POLY-PRO.
FT DOMAIN 754 757 POLY-PRO.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 931 AA; 99537 MW; B0D99D594209F125 CRC64;

Query Match 27.4%; Score 1493.5; DB 1; Length 931;
Best Local Similarity 35.7%; Pred. No. 1.4e-88;
Matches 374; Conservative 145; Mismatches 353; Indels 177; Gaps 32;

Qy 6 LLLYFTLLHFAGAGFPEDSEPISISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMN 65
||| : | ||| ||:| |: | | | : : | ||| : :| | ||| : :| |
Db 13 LLLLLSSLPQAQAAFPQDPPTPLLTSDLQGASPSSWFRGLEDDAVAAEL-GLDFQRFLT 71

Qy 66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSQRADVDTCRMKGKHDECHNF 124
|| :|||||:::|:| : | : | |||:|:| ::| | :||| :|||:|:|:
Db 72 RTLLVAARDHVFSFDLQAQEEGEGLVPNKFLTWSQ--DMENCAVRGKLTDECNYIRVL 129

Qy 125 LKKNDDALFVCGTNAFNPSRNPKMDTLEPGDEFSGMARCPTYDAKHANVALFADGKL 184
: | | |||:|:| | ||:| : :| : ||| |||:|| : |||:|:| |||
Db 130 VPWNSQTLLACGTNSFPMCRSYGITSLQQEGEELSGQARCPFDATQSTVAIFAEGLYS 189

Qy 185 ATVTDFLAI DAVIYRSLGESPTLRTVKHD SKWLKEPYFVQAVDYGDYIYFFFREIAVEYN 244
|| | | |||:|||| | ||: | :||||:||:|| | ::|:|||:|||:
Db 190 ATAADFQASDAVVYRSLGPQPPLRSAKYDSKWLREPHFVYALEHGEHVYFFFREVSVEDA 249

Qy 245 TMGKVVFPRAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTDVIR 304
:||| | |||:||| | |||| | ||: | ||| |||:||| |||:||:| :|
Db 250 RLGRVQFSRVARVCKRDGGSPRALDRHWTSFLKRLNCSVGDSTFYFDVLQSLTGPVN 309

Qy 305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDERVPKP 364
::|| : |:| | |||:|||:|:|| | |:|||:| | | ||| :||| |
Db 310 LHGRSALFGVFTTQTNSIPGSAVCAFYLDDIERGFEGKFKEQRSLDGAWT PVS EDKVPSP 369

Qy 365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFRLTMVRYRLTKIA 424
||| ||| : | ::| : | ||| | ||| |||:| ||| :||| | | | |||:

Db	370	RPGSCAGVGAAASFSSQDLPDDVLLFIKAHPPLDPAVPPATHQP-LLTLTSRALLTQVA	428
Qy	425	VDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVED	484
:: : : :: : : : :			
Db	429	VDGMAGPHRNTTVLFLGSNDGTVLKVLPP-GGQSLGSEPIVLEEIDAYSHARCS--GKRS	485
Qy	485	----KrimGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKTCIASRDYPYCGWIKEGG	540
: : : : : : : : :			
Db	486	PRAARRIIGLELDTEGHRLFVAFPGCIVYLSLSRCARHGACQRSCLASLDPYCGWHRSG	545
Qy	541	ACSHLSPNSRLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTSDDSTAQEGLYE-S	599
: :			
Db	546	CMSIRGP-----GGTD-----VDLTGNQES-----TEHGDCQDGATGS	578
Qy	600	RGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLGKHDQLPVTLLAIAVILAF	659
: : : : : :			
Db	579	QSGPGDSAY-----GVRRDLSPASASRSIPIPLLLACVAAF	615
Qy	660	VMGAVFGITVYCVCVDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSCKDPKP	719
: : : : :			
Db	616	ALGASVSGLLVSCAC--RRAN---RRRSKDIETPGLPRPLSLRSLARLHGGPEPPPPP	669
Qy	720	---EAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSRE	776
: : : : : :			
Db	670	KDGDAAQTPQLYTTFLPPPDGGSPP-----ELACLPTPETTPELPVKHLRASGG-P	719
Qy	777	WERNQNLINACT-KDMPPMGSPVIPTDLP---LRASPISHPSVVVLPIITQQ---GYQH--	827
:			
Db	720	WEWNQNGNNASEGPGRPPRGCSGAGGPAPRVLVRPPPGCPGQAVEVTITLEELLRYLHGP	779
Qy	828	-----EYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSPNHLGVNLVENL	874
: : :			
Db	780	QPPRKGSSEPLASAPFTSRPPASEPGASLFVD-----SSPMPRDGVPPL-RL	824
Qy	875	DSDLPPK---VPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQ	930
: : : : : :			
Db	825	D-VPPEGKRAAPSGRPALSAPAPRLG-VGGSRRL-----PFPT-----HR	862
Qy	931	ATTIJKRNNTNSSNSHLSRNQSFGRGDNPPAPQRVDS--IQVHSSQPSGQAVTVSRQPS	988
: : :			
Db	863	A-----PPGLLTRVPSGGPARYSGGPGRHLLYLGR-PE	894
Qy	989	LNAYNSLTRSGLKRTPSLKPDV--PPKPS	1015
: : : : : : :			
Db	895	GHRGRSLKRVDVKSPLSPKPPLASPPQPA	923

RESULT 8

SM6C_RAT
ID SM6C_RAT STANDARD; PRT; 960 AA.
AC Q9WTL3; Q9WTM6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Semaphorin 6C precursor (Semaphorin Y) (Sema Y)
GN SEMA6C OR SEMAY.
OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS SEMA Y-L AND SEMA Y-S).
RC STRAIN=Sprague-Dawley; TISSUE=Muscle;
RX MEDLINE=99160821; PubMed=10049528;
RA Kikuchi K., Chedotal A., Hanafusa H., Ujimasa Y., de Castro F.,
RA Goodman C.S., Kimura T.;
RT "Cloning and characterization of a novel class VI semaphorin,
RT semaphorin Y.";
RL Mol. Cell. Neurosci. 13:9-23(1999).
CC -!- FUNCTION: SHOWS GROWTH CONE COLLAPSING ACTIVITY ON DORSAL ROOT
CC GANGLION (DRG) NEURONS IN VITRO. MAY BE A STOP SIGNAL FOR THE DRG
CC NEURONS IN THEIR TARGET AREAS, AND POSSIBLY ALSO FOR OTHER
CC NEURONS. MAY ALSO BE INVOLVED IN THE MAINTENANCE AND REMODELING OF
CC NEURONAL CONNECTIONS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Sema Y-L;
CC IsoId=Q9WTL3-1; Sequence=Displayed;
CC Name=Sema Y-S;
CC IsoId=Q9WTL3-2; Sequence=VSP_006048;
CC -!- TISSUE SPECIFICITY: Expressed in many regions of the developing
CC nervous system, probably in neurons and their precursors, but also
CC in nonneuronal tissue such as immature muscle and dermis. In adult,
CC strong expression in the skeletal muscle and moderate expression
CC in the brain, where cerebellum shows the highest expression. Also
CC expressed in almost all areas of the CNS.
CC -!- DEVELOPMENTAL STAGE: DETECTED AT E12 AND FOUND AT MARKEDLY
CC INCREASED LEVELS AT E15 AND E18 IN BOTH THE HEAD AND THE BODY. AT
CC BIRTH THE LEVEL DECREASES SIGNIFICANTLY.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB000817; BAA76293.2; -.
DR EMBL; AB014074; BAA76295.1; -.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00630; Sema; 1.
KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
KW Developmental protein; Alternative splicing.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 960 SEMAPHORIN 6C.
FT DOMAIN 24 635 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 636 656 POTENTIAL.
FT DOMAIN 657 960 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 234 541 SEMA.

FT DOMAIN 693 699 POLY-PRO.
 FT DOMAIN 783 786 POLY-PRO.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 436 436 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 586 617 Missing (in isoform Sema Y-S).
 FT /FTId=VSP_006048.
 SQ SEQUENCE 960 AA; 102610 MW; C88293C5607E6086 CRC64;

Query Match 27.4%; Score 1491; DB 1; Length 960;
 Best Local Similarity 35.1%; Pred. No. 2.1e-88;
 Matches 374; Conservative 149; Mismatches 363; Indels 180; Gaps 32;

Qy 6 LLLYFTLLHFAGAGFPEDSEPIISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMN 65
 ||| | | ||::| |: | | | | || : : || | : :|||
 Db 11 LLLLLLSPQAQTAFPQDPPIPLLTSDLQGTSPSSWFRGLEDDAVAAEL-GLDFQRFLTLN 69

Qy 66 GTLYIAARDHIYTVDIDTSHT-EEIYCSKKLTWKSRQADVDTCRMKGKHDECHNFIKVL 124
 || :||||::: |: | : | ||::|: | :: | :||| ||::|:||:|||
 Db 70 RTLLVAARDHVFSFDLQAQEEGEGLVPNKFLLWRSQ--DMENCAVRGKLTDECNYIRVL 127

Qy 125 LKKNDDALFVCGTNAFPSCRNYKMDTLEPGDEFSGMARCPYDAKHANVALFADGKLYS 184
 : : | | ||::|:|| |::| : |: |:| || ||::|:|| : ||: |:| |||
 Db 128 VPWDSQTLLACGTNSFPVCRSYGITSLQQEGEELSGQARCPFDATQSTVAISAEGSLYS 187

Qy 185 ATVTDFLAIDAVIYRSLGESPTLRTVKHD SKWLKEPYFVQAVDYGYDIYFFFREIAVEYN 244
 || | | | ||::|:|||| | ||: |:|||::|:|| | ::::| |::|:||||::|:
 Db 188 ATAADFQASDAVVYRSLGPQPPLRSAKYDSKWLREPHFVYALEHGDHVYFFFREVSVEDA 247

Qy 245 TMGVVFPRVAQVCKNDMGGSQLRKQWTSFLKARLNCSVPGDHFYFNILQAVTDVIR 304
 ::|: | | ||::|:|| | ||::|: | || | |||:|:| | ||| | ::|| |
 Db 248 RLGRVQFSRVARVCKRDMMGSPRALDRHWTSLKLRLNCVPGDSTFYFDVLQLSLGPVN 307

Qy 305 INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWT PVPDERVPKP 364
 ::|| : |:| | |||:|:|| | :|| | |:|||:| | | ||| | ::|| |
 Db 308 LHGRSALFGVFTTQTN SIPGSAVCAFYLDDIERGFEGKFKEQRSLDGAWTPVSEDKVPSP 367

Qy 365 RPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIA 424
 ||| ||| : ::| : ||| | ||| |||:| ||| :| | | | |||:|||
 Db 368 RPGSCAGVGAALFSSSQDLPDDVLLFIKAHPLLDPAVPPATHQP-LLTLTSRALLTQVA 426

Qy 425 VDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGLNDSLFLLEMSVYNSEKCSYDGVED 484
 || | ||::| | ||:|| | :|| | | | : | ||: |: | :|| |
 Db 427 VDGMAGPHRNTTVLFLGSNDGTVLKVLPP-GGQSLGPEPIILEEIDAYSHARCS--GKRS 483

Qy 485 ----KRIMGMQLDRASSSLYVAFSTCVIKVPLGRcerHGKCKTCIASRDPYCGWIKEGG 540
 ::||:|:|| |:|| | ::| : | ||| ||| | ::|:| | ||| : |
 Db 484 PRAARRIIGLELDTEGHRLFVAFPGCIVYLSRCARHGACQRSCLASLDPYCGWHRFRG 543

Qy 541 ACSHLSPNSRLTFEQDIE-RGNTDGL--GDCHNSFVALN---GHSSLL----PSTTT 588
 : | |::| | : | || : | | : | | : | | | : | | | : |
 Db 544 CVNIRGPGG----TDVDLGNQESMEHGDCQDGATGSQSGPGDSAYVLLGPGPSPETPS 598

Qy 589 SDSTAQEYESRGGMWDWKHLLSPDSTDPLGAVSSHNNQDKKGVIRESYLYKGHDQLVPV 648
 | | | | : | | || | : | | : | : | : |
 Db 599 SPSDAHPGPQS-----STLGA-----HTQGVRRDLSPASASRSIPI 634

Qy	649	TLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVQRKELTHSRRGSMSVTKLSQL	708
	: : : : : ::: : :		
Db	635	PLLLACVAAAFALGASVSGLLVSCAC--RRAN---RRRSKDIETPGLPRPLSLRSIARL	688
Qy	709	FGDTQSKDPKP---EAILTPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQ	765
	: :: : : : :		
Db	689	HGGGPEPPPPPDKDGAQTPQLYTTFLPPPEGGSPP-----ELACLPTPETTPELP	739
Qy	766	QKRKPSRGSREWERNQNLLINACTKDMPPMGSPVIPTDLP---LRASPShIPSVVVLPIQ	822
	: :		
Db	740	VKHLRASGG-PWEWNQNGNNASEGPGRPRGCSAAGGPAPRVLVRPPPGCPQEVEVTTL	798
Qy	823	Q---GYQH-----EYVDQPKMSEVAQMALEDQAATLEYKTIKEHLSSKSP	864
	: : :		
Db	799	EELLRYLHGPQPPRKGSEPLASAPFTSRPPASEPAGAALFVD-----SSPMP	844
Qy	865	NHGVNLVENLDSLPP-----KVPQREASLGPPGASLSQTGLSKRLEMHHSSSYG	913
	: : : :		
Db	845	R-----DCVPPLRLDVPPDGKRAAPSGRPALSAPAPRLGVSG-SRRL-----	885
Qy	914	VDYKRSYPTNSLTRSHQATTLKRNNTNSSNSHLSRNQSFGRGDNPPPAPQRVDS--IQV	971
	: : :		
Db	886	-----PFPT-----HRA-----PPGLLTRVPSGGPSR	907
Qy	972	HSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDV--PPKPS	1015
	: : : : : : : :		
Db	908	YSGGPGRHLLYLGR-PDGHRGRSLKRVDVKSPLSPKPLATPPQPA	952

RESULT 9

SM1A_SCHAM
ID SM1A_SCHAM STANDARD; PRT; 730 AA.
AC Q26473;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Semaphorin 1A precursor (Semaphorin-I) (Sema I) (Fasciclin IV)
GN SEMA-1A OR FAS4.
OS Schistocerca americana (American grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridocephala;
OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
OX NCBI_TaxID=7009;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93040225; PubMed=1418998;
RA Kolodkin A.L., Matthes D.J., O'Connor T.P., Patel N.H., Admon
RA Bentley D., Goodman C.S.;
RT "Fasciclin IV: sequence, expression, and function during growth
RT guidance in the grasshopper embryo.";
RL Neuron 9:831-845(1992).
CC -!- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: DYNAMICALLY EXPRESSED ON A SUBSET OF A
CC PATHWAYS IN THE DEVELOPING CNS AND ON CIRCUMFERENTIAL BANDS
CC EPITHELIAL CELLS IN DEVELOPING LIMB BUDS.
CC -!- SIMILARITY: Belongs to the semaphorin family.

|||| | ||| || :: |||:|||:| || : :: ||||||:||||||| ||||
 Db 221 FFRETAVEYINCWKAIYSRVARVCKHDKGPHQFGDR-WTSFLKSRNLNCSPGDYPFYFN 279
 Qy 295 ILQAVTDVIRIN-GRDV---VLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPD 350
 :|: :|:| ||| | : |:|| ||| |||||: | | | | | |||:: :
 Db 280 EIQSTSDDIIEGNYGGQVEKLIYGVFTTPVNSIGGSACAFSMKSILESDGPFKEQETMN 339
 Qy 351 STWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPW 410
 | | || :||:||| | | | || :||:|:| | ||| |||: | |||
 Db 340 SNWLAVPSLKVPEPRPGQCVCND-----SRTLPDVSNFVKSHTLMDEAVPAFFTRPI 391
 Qy 411 FLRTMVRYRLTKIAVD---TAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLN---- 461
 :| :|| | ||| | | : : |:|:|:| :| ||| :|| :
 Db 392 LIRISLQYRFTKIAVDQQVRTPDG--KAYDVLFIGTDDGKVIKAL---NSASFDSSTV 445
 Qy 462 DSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC--ERHG 519
 ||: :||: | | | | : :|| | | | | : :| ||| :|| :
 Db 446 DSVVIEELQVLP-----PGVPVKNLVVRMDGDDSKLVVVSDEILAIKLHRCGSDKIT 499
 Qy 520 KCKKTCIASRDPYCGWIKEGGACSHL-SPN---SRLTFEQDIERGNTDGLGDCHNSFVAL 575
 |::|:::| ||| | | :|:|:| :| | | | | :| :
 Db 500 NCRE-CVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEHKACGGRPQTEIV- 557
 Qy 576 NGHSSLLPSTTSDDSTA-----QEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNNQ 628
 :| :|: | :|: | | :| :| :| :| :| :| :| :| :|
 Db 558 ---ASPVPTQPTTKSSGDPVHSIHQAEEPE---IDNEIVIGVDDSNVIPNTLAEINHA 610
 Qy 629 DKKGVIRESYLKHDQLVPV---TL-LAI-----AVILAFVMGAVFS 666
 | | | :|: | | :|| | :| :| :| :| :| :| :|
 Db 611 GSK-----LPSSQEKLPIYTAELTIAIVTSCLGALVVGFIISGFLFS 652

RESULT 10

SM1A_DROME

ID SM1A_DROME STANDARD; PRT; 771 AA.
 AC Q24322;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 1A precursor (Semaphorin-I) (Sema I).
 GN SEMA-1A OR DSEMA-I OR CG18405.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriodea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=94094332; PubMed=8269517;
 RA Kolodkin A.L., Matthes D.J., Goodman C.S.;
 RT "The semaphorin genes encode a family of transmembrane and secreted
 growth cone guidance molecules.";
 RL Cell 75:1389-1399(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;

RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).

CC -!- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED BY SUBSETS OF NEURONS AND MUSCLES.
CC -!- DEVELOPMENTAL STAGE: EXPRESSION BEGINS AROUND STAGE 10, PRIMARILY
CC IN THE DEVELOPING CNS. IN STAGE 16 EMBRYOS, IT IS EXPRESSED AT
CC HIGHEST LEVELS THROUGHOUT THE CNS, AND WEAK EXPRESSION IS SEEN IN
CC PORTIONS OF THE PERIPHERAL NERVOUS SYSTEM, MOST CLEARLY IN THE
CC LATERAL SENSORY CLUSTERS.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.

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CC
 DR EMBL; L26082; AAA88789.1; -.
 DR EMBL; AE003621; AAF52696.1; -.
 DR FlyBase; FBgn0011259; Sema-1a.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Developmental protein; Transmembrane; Glycoprotein;
 KW Neurogenesis.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 771 SEMAPHORIN 1A.
 FT DOMAIN 21 608 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 609 629 POTENTIAL.
 FT DOMAIN 630 771 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 210 519 SEMA.
 FT DOMAIN 689 694 POLY-PRO.
 FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 771 AA; 86935 MW; 752E7DD516F32DA5 CRC64;

Query Match 17.1%; Score 932.5; DB 1; Length 771;
Best Local Similarity 35.0%; Pred. No. 1.7e-52;
Matches 219; Conservative 106; Mismatches 213; Indels 87; Gaps 20;

Qy 67 TLYIAARDHIYTVDIDTSHTEIYCSSLKLTWKSQRQADVDTCRMKGKHKDECHNFIKVLLK 126
 :| | ||: :: :| :: :|| | | :| | | :|| :: | | :||:|||||:
 Ph 57 SILICAPNTYENLST HDLYEOORLIVWTSRDPDTKMCILVKCKDFFACONYXTRIMV 111

Qy 127 KNDDALFVCGTNAFNPSRNYKMD---TLEPGDFSGMARCPYDAKHANVALFADGKL 182
: |||||||: | | | : | | | : | | | | | | : | | | | | | | | | | | | | | | |

Qy 183 YSATVTDLAI DAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAVE 242
|| || || | :||| |::||| | | || : ||::||||| |||

Qy 303 IR---INGRDVVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWT PVPD 358

Qy 359 ERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFRLTMVRY 418

Db 343 AKVPDPRPGSC-----HNDRALPDPTLNFIKTHSLMDENVPAFFSQPILVRTSIY 394
Qy 419 RLTKIAVD----TAAGPYQNHTVVFLGSEKGIIILKFL-ARIGNSGFLNDSLFLEEMS VYN 473

RESULT 11

SM3A_RAT
ID SM3A_RAT STANDARD; PRT; 772 AA.
AC Q63548;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Semaphorin 3A precursor (Semaphorin III) (Sema III).
GN SEMA3A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=97073089; PubMed=8915837;
RA Giger R.J., Wolfer D.P., De Wit G.M.J., Verhaagen J.;
RT "Anatomy of rat semaphorin III/collapsin-1 mRNA expression and
RT relationship to developing nerve tracts during neuroembryogenesis.";
RL J. Comp. Neurol. 375:378-392(1996).
CC -!- FUNCTION: MAY BE INVOLVED IN GUIDING GROWING AXONS TOWARDS THEIR
CC TARGETS BY FORMING A MOLECULAR BOUNDARY THAT INSTRUCTS AXONS TO
CC ENGAGE IN THE FORMATION OF SPECIFIC NERVE TRACTS. BINDS TO
CC NEUROPILIN.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- DEVELOPMENTAL STAGE: AT E-11, EXPRESSION WAS RESTRICTED TO THE
CC OLFACTORY PIT, THE BASAL AND ROSTRAL SURFACE OF THE TELENCEPHALIC
CC VESICLE, THE EYE ANLAGE, THE EPITHELIUM OF RATHKE'S POUCH, AND
CC SOMITES. AT LATER DEVELOPMENTAL STAGES, IT WAS WIDELY DISTRIBUTED
CC IN NEURONAL AS WELL AS IN MESENCHYMAL AND EPITHELIAL STRUCTURES
CC OUTSIDE THE NERVOUS SYSTEM. AFTER BIRTH, MESENCHYMAL LEVELS
CC DECREASED RAPIDLY AND EXPRESSION BECAME RESTRICTED TO SPECIFIC
CC SETS OF NEURONS IN THE CNS. IN THE MATURE CNS, IT IS DETECTABLE IN
CC MITRAL CELLS, NEURONS OF THE ACCESSORY BULB AND CEREBRAL CORTEX,
CC CEREBELLAR PURKINJE CELLS, AS WELL AS A SUBSET OF CRANIAL AND
CC SPINAL MOTONEURONS.

CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy
 CC third of the protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC -----
 DR EMBL; X95286; CAA64607.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 772 SEMAPHORIN 3A.
 FT DOMAIN 240 538 SEMA.
 FT DOMAIN 577 665 IG-LIKE C2-TYPE.
 FT DOMAIN 728 770 ARG/LYS-RICH (BASIC).
 FT DISULFID 650 723 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 772 AA; 88808 MW; 240907812FF9F2D2 CRC64;

Query Match 15.7%; Score 858; DB 1; Length 772;
 Best Local Similarity 32.3%; Pred. No. 1.1e-47;
 Matches 209; Conservative 104; Mismatches 251; Indels 84; Gaps 20;

Qy	47 GRNTTQRHRLDIQMIMIMNGT-----	LYIAARDHIYTVDIDT	83
	: : : ::	: : :: ::	
Db	25 GKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHIFS FNL--		82
Qy	84 SHTEEIYCSKKLTWKSQRADVTCRMKGKH-KDECHNFIKVLLKKNDALFVCGTNAFP	142	
	: : : : :		
Db	83 ---VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGAFHP	139	
Qy	143 SCR----NYKMDTLEPPGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFAIDA	195	
	:: : : : : :		
Db	140 ICTYIEVGHHPEDNIFKLQDSHFENGRGKSPYDPKLLTASLLIDGELYSGTAADFMGRDF	199	
Qy	196 VIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----	VDYGDYIYFFFREIAVEYNTMGK	248
	: : : : : : : : :		
Db	200 AIFRTLGHHHPIRTEQHDSRWLNDPRFISAHЛИPESDNPEDDKVYFFFRENAIDGEHSGK	259	

Qy 249 VVFPRVAQVCKNDMGGSQLRVLKEQWTSFLKARLNCSVPG----DSHFYFNILQAVTDVIR 304
 | : | : || | | | | : || : || | | | | | | | | | | | | | | | | | | | | | |
 Db 260 ATHARIGQICKNDFGG-HRSLVNWKTTFLKARLICSVPGPNGIDTHF----DELQDVFL 313

 Qy 305 INGRD---VVLATFSTPYNSIPGSACAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER 360
 | : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 314 MNSKDPKNPIVYGVFTTSSNIFKGSAVCMSMSDVRVFLGPYAHRDGPNYQWVPY-QGR 372

 Qy 361 VPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL 420
 | | | | | | | : : : : | | | : | : | | | | | | | | | | | | | | | | | | |
 Db 373 VPYPRPGTCP-SKTFGGFDSTKDLPPDDVITFARSHPAMYNPVFPINNRPIMIKTDVNYQF 431

 Qy 421 TKIAVDTAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLFLLEEMSVYNSEKCSYD 480
 | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 432 TQIVVDRVDAEDGQYDVMFIGTDVGTVLKVSVPKETWHDLLEEVLLLEEMTVFR----- 484

 Qy 481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCRERHGKCKKTCIASRDPYCGWIKEGG 540
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 485 --EPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECLARDPYCAW--DGS 540

 Qy 541 ACSHLSPNS-RLTFEQDIERGNTDGLGDC----HNSFVALNGHS--SSLLPSTTSDST 592
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 541 SCSRYFPTAKRRTRRQDIRNG--DPLTHCSDLQHHDNH---HGHSLEERIIYGVENSSTF 595

 Qy 593 AQEGYESRGGMQLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLK 640
 | : | : | : | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 596 LECSPKSQRALVYWFQRRNEDRKEEI-RVGDHIIRTEQGLLLRSIQLQK 642

RESULT 12

SM3A_MOUSE

ID SM3A_MOUSE STANDARD; PRT; 772 AA.
 AC 008665; Q62180; Q62215;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Semaphorin 3A precursor (Semaphorin III) (Sema III) (Semaphorin D)
 DE (Sema D).
 GN SEMA3A OR SEMAD OR SEMD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMR1; TISSUE=Embryo;
 RX MEDLINE=95267431; PubMed=7748561;
 RA Pueschel A.W., Adams R.H., Betz H.;
 RT "Murine semaphorin D/collapsin is a member of a diverse gene family
 RT and creates domains inhibitory for axonal extension.";
 RL Neuron 14:941-948(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97470885; PubMed=9331345;
 RA Taniguchi M., Yuasa S., Fujisawa H., Naruse I., Saga S., Mishina M.,
 RA Yagi T. ;

RT "Disruption of semaphorin III/D gene causes severe abnormality in peripheral nerve projection.";
RL Neuron 19:519-530(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Kimura T., Fishman M.C.;
RT "cDNA sequence of mouse collapsin/semaforin III.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 107-772 FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=95267432; PubMed=7748562;
RA Messersmith E.K., Leonardo E.D., Shatz C.J., Tessier-Lavigne M.,
RA Goodman C.S., Kolodkin A.L.;
RT "Semaphorin III can function as a selective chemorepellent to pattern
RT sensory projections in the spinal cord.";
RL Neuron 14:949-959(1995).
CC -!- FUNCTION: Play a role in growth cones guidance. May function to
CC pattern sensory projections by selectively repelling axons that
CC normally terminate dorsally.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED EARLY IN EMBRYONIC DEVELOPMENT
CC (E11) IN DISTINCT REGIONS OF THE NEUROECTODERM AND MESODERM.
CC EXPRESSION BECAME MORE EXTENSIVE AT LATER STAGES.
CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy
CC third of the protein.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
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DR EMBL; X85993; CAA59985.1; -.
 DR EMBL; D85028; BAA19773.1; -.
 DR EMBL; L41541; AAL77611.1; -.
 DR EMBL; BC057588; AAH57588.1; -.
 DR EMBL; L40484; AAA73934.1; -.
 DR PIR; I48747; I48747.
 DR PIR; I58169; I58169.
 DR MGD; MGI:107558; Sema3a.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 772 SEMAPHORIN 3A.
 FT DOMAIN 240 538 SEMA.
 FT DOMAIN 579 665 IG-LIKE C2-TYPE.
 FT DOMAIN 728 770 ARG/LYS-RICH (BASIC).
 FT DISULFID 650 723 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 193 193 D -> N (IN REF. 5).
 FT CONFLICT 207 207 H -> D (IN REF. 1).
 FT CONFLICT 253 253 D -> G (IN REF. 1).
 FT CONFLICT 352 352 F -> L (IN REF. 5).
 FT CONFLICT 403 403 A -> G (IN REF. 1).
 FT CONFLICT 571 572 QH -> ED (IN REF. 1).
 FT CONFLICT 616 620 EDRKE -> RRSKR (IN REF. 1).
 FT CONFLICT 623 623 R -> K (IN REF. 5).
 SO SEQUENCE 772 AA: 88799 MW: E89A08528B10AEC3 CRC64;

Query Match 15.7%; Score 853; DB 1; Length 772;
Best Local Similarity 32.2%; Pred. No. 2.3e-47;
Matches 208; Conservative 102; Mismatches 257; Indels 78; Gaps 18;

Qy	47	GRNTTQRHRLDIQMIMIMNGT-----LYIAARDHIYTVDIDT	83
		:: : : :: : : :: ::	
Db	25	GKNNVPRLKLSYKEMLESNNVITFNGLANSYYHTFLLDEERSRLYVGAKDHIFSNL--	82
Qy	84	SHTEEIYCSKKLTWKSQADVDTCRMKGKH-KDECHNFIKVLLKKNDALFVCGTNAPNP	14
		. : : : : :	
Db	83	--VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLEAYNQTHLYACGTGAFHP	13
Qy	143	SCR----NYKMDTLEPGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLAIDA	19

Db	140 ICTYIEVGHHPEDNIFKLQDSHFENGGRGKSPYDPKLLTASLLIDGELYSGTAADFMGRDF	199
Qy	196 VIYRSLGESPTLRTVKHDSKWLKEPYFVQA-----VDYGDYIYFFFREIAVEYNTMGK	248
Db	200 AIFRTLGHHHPIRTEQHDSRWLNDPRFISAHLIPESDNPEDDKVYFFFRENAIDGEHSGK	259
Qy	249 VVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPG---DSHFYFNILQAVTDVIR	304
Db	260 ATHARIGQICKNDFGG-HRSLVNVKWTTFKLKARLICSVPGPNGIDTHF----DELQDVFL	313
Qy	305 INGRD---VVLATFSTPYNSIPGSAVCAYDMLDIASVFTGRFKEQKSPDSTWTPVPDER	360
Db	314 MNSKDPKNPIVYGVFTTSSNIFKGSAVCMSDVRVFLGPYAHRDGPNYQWVPY-QGR	372
Qy	361 VPKRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRL	420
Db	373 VPYPRPGTCP-SKTFGGFDSTKDLPPDDVITFARSHPAMYNPVFPINNRPIMIKTDVNYQF	431
Qy	421 TKIADVTAAGPYQNHTVVFLGSEKGIILKFLARIGNSGFLNDSLLEEMSVYNSEKCSYD	480
Db	432 TQIVVDRVDAEDGQYDVMFIGTDVGTVLKVSVPKETWHDLEEVILLEMTVFR-----	484
Qy	481 GVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGG	540
Db	485 --EPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECLARDPYCAW--DGS	540
Qy	541 ACSHLSPNS-RLTFEQDIERGNTDGLGDCHNSFVALNGHSSL---LPSTTSDSTAQE	595
Db	541 SCSRYFPTAKRRTRRQDIRNG--DPLTHCSDLQHHDNHGPSLEERIIYGVENSTFLEC	598
Qy	596 GYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLK	640
Db	599 SPKSQRALVYWQFQRRNEDRKEEI-RMGDHIIIRTEQGLLLRSLOK	642

RESULT 13

SM3A_HUMAN

ID SM3A_HUMAN STANDARD; PRT; 771 AA.
 AC Q14563;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 3A precursor (Semaphorin III) (Sema III).
 GN SEMA3A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=94094332; PubMed=8269517;
 RA Kolodkin A.L., Matthes D.J., Goodman C.S.;
 RT "The semaphorin genes encode a family of transmembrane and secreted
 growth cone guidance molecules.";
 RL Cell 75:1389-1399(1993).

RN [2]
RP SEQUENCE OF 1-37 FROM N.A.
RA Woessner J., Minx P., Hinds K., Strowmatt C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 39-182 FROM N.A.
RA Rohlffing T., Tin-Wollam A.M., Duckels G.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH
CC CONES. COULD SERVE AS A LIGAND THAT GUIDES SPECIFIC GROWTH CONES
CC BY A MOTILITY-INHIBITING MECHANISM. BINDS TO THE COMPLEX
CC NEUROPILIN-1/PLEXIN-1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy
CC third of the protein.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
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CC -----
DR EMBL; L26081; AAA65938.1; -.
DR EMBL; AC004451; -; NOT_ANNOTATED_CDS.
DR EMBL; AC004848; AAC78622.1; -.
DR PIR; D49423; D49423.
DR Genew; HGNC:10723; SEMA3A.
DR MIM; 603961; -.
DR GO; GO:0005576; C:extracellular; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR001627; Sema.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
KW Developmental protein; Glycoprotein.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 771 SEMAPHORIN 3A.
FT DOMAIN 240 538 SEMA.
FT DOMAIN 580 664 IG-LIKE C2-TYPE.
FT DOMAIN 727 769 ARG/LYS-RICH (BASIC).
FT DISULFID 649 722 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 590 590 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 771 AA; 88889 MW; 9985F8D3EAED8456 CRC64;

Query Match 15.6%; Score 852.5; DB 1; Length 771;
 Best Local Similarity 32.1%; Pred. No. 2.5e-47;
 Matches 208; Conservative 106; Mismatches 250; Indels 83; Gaps 20;

 44 HKPGRNTTQRHRLDIQMIMIMNGT-----LYIAARDHIYTVD 80
 :: |::| | :| : ::| | :| :|||::|
 22 YQNGKNNVPRLKLSYKEMLESNNVITFNGLANSYYHTFLLDEERSRLYVGAKDHIFSD 81

 81 IDTSHTEEIYCSKKLTWKSQADVDTCRMKGKH-KDECHNFIKVLLKKNDALFVCGTNA 139
 :| :| | :| | | :| ||| ||| | | | :| ||| |
 82 L-----VNIKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGA 136

 140 FNPSCR----NYKMDTLEPGDEF--SGMARCPYDAKHANVALFADGKLYSATVTDFLA 192
 |::| | ::| | :| :| :| :| ||| | :| ||| :| |
 137 FHPICTYIEIGHHPEDNIFKLENSHFENGGRGKSPYDPKLLTASLLIDGELYSGTAADFMG 196

 193 IDAVIYRSLGESPTLRTVKHDSKWLEPYFVQA-----VDYGDYIYFFFREIAVEYNT 245
 | |::|:|| | :|| | :|||:|| | :| | | :| ||| | |:
 197 RDFAIFRTLGHHPIRTEQHDSRWLNDPKFISAHLISESDNPEDDKVYFFFRENAIDGEH 256

 246 MGKVVFPRAVQCKNDMGGSSQRVLEKQWTSFLKARLNCSVPG---DSHFYFNILQAVTD 301
 || |:|:|| | | | | :| :||| | | | | | :| | :|
 257 SGKATHARIGQICKNDFGG-HRSLVNVKWTTFLKARLICSVPGPNGIDTHF----DELQD 310

 302 VIRINGRD---VVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPVP 357
 | | :| :| | | | | :| | | | | | | | | | | | | |
 311 VFLMNFKDPKPNPVYGVFTSSNIFKGSAVCMSDVRVFLGPYAHRDGPNYQWVPPY- 369

 358 DERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVR 417
 ||| | | | | | | :| :| :| | | :| | | | | | | | | |
 370 QGRVPYPRPGTCP-SKTFGGFDSTKDLPPDDVITFARSHPAMYNPVPMNNRPIVIKTDVN 428

 418 YRLTKIAVDTAAAGPYQNHTVVFLGSEKGIIILKFLARIGNSGFLNDSLFLLEMSVYNSEKC 477
 | :| :| | | | | :| :| :| | | | | | | | | | | | | |
 429 YQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSIPKETWYDLEEVILLEEMTVFR--- 484

 478 SYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRCERGKCKTCIASRDPYCGWIK 537
 | | | | :| | | | | | | | | | | | | | | | | | | | |
 485 -----EPTAISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAW-- 537

 538 EGGACSHLSPNS-RLTFEQDIERGNTDGLGDC---HNSFVALNGHS--SSLNPSTTSD 590
 | | | | | | :| | | | | | | | | | | | | | | | | | |
 538 DGSACSRYSFPTAKRRTRRQDIRNG--DPLTHCSDLHHHDNH---HGHSPPEERIYGVENSS 592

 591 STAQEYESRGGMULDWKHLLSDPDSTDPLGAVSSHQDKKGVIRES 637
 | | | | | | :| | | | | | | | | | | | | | | | | | |
 593 TFLCSPKSQRALVYWFQRRNEERKEEI-RVDDHIIRTQGLLLRS 638

RESULT 14

SM1A TRICF

ID SM1A_TRICF STANDARD; PRT; 712 AA.
AC Q26972;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Semaphorin 1A precursor (Semaphorin-I).

GN SEMA-1A OR TSEMA-I.
 OS Tribolium confusum (Confused flour beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tribolium.
 OX NCBI_TaxID=7071;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=94094332; PubMed=8269517;
 RA Kolodkin A.L., Matthes D.J., Goodman C.S.;
 RT "The semaphorin genes encode a family of transmembrane and secreted
 growth cone guidance molecules.";
 RL Cell 75:1389-1399(1993).
 CC --!- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE.
 CC --!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC --!- SIMILARITY: Belongs to the semaphorin family.
 CC --!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; L26080; AAA16609.1; -.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Developmental protein; Transmembrane; Glycoprotein;
 KW Neurogenesis.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 712 SEMAPHORIN 1A.
 FT DOMAIN 21 601 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 602 622 POTENTIAL.
 FT DOMAIN 623 712 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 213 506 SEMA.
 FT DOMAIN 470 473 POLY-VAL.
 FT DOMAIN 612 616 POLY-VAL.
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 712 AA; 79751 MW; C0734FE5B9C09FE3 CRC64;

 Query Match 15.5%; Score 845; DB 1; Length 712;
 Best Local Similarity 28.9%; Pred. No. 6.8e-47;
 Matches 230; Conservative 130; Mismatches 270; Indels 166; Gaps 30;

 Qy 12 LLHFAGAGFPEDSEPI----SISHGNYTKQYPVFVGHKPGRNTTQRHRLDIQMIMIMN- 65
 |: | |: | : |: ::| | | | ::::|

Db 12 LIALCHAWMPDSSSKLINHFKSVESKSFT-----GNATFPDH----FIVLNU 54
Qy 66 --GTLYIAARDHIYTVDI-DTSHTEIYCSKKLTWKSQRADVDTCRMKGKHKDECHNFIK 122
Db 55 DETSILVGGRNRVYNLSIFDLSERK---GGRIDWPSSDAHGQLCILKGKTDDDCQNYIR 110
Qy 123 VLLKKNDDALFVCGTNAFNPSRNPKMDTLEPFGD-EFSGMARCPTYDAKHANVALFADGK 181
Db 111 ILYSSEPGKLVICGTNSYKPLCRTYAFKEKGKYLVEKEVEGIGLCPYNPEHNSTSVDNGQ 170
Qy 182 LYSATVTDFLAI DAVIYRSLGESPTLRTVKHDSKWLKEPYFVQAVDYGDYIYFFFREIAV 241
Db 171 LFSATVADFSGGDPLIYRE----PQRTESDLKQLNAPNFVNNSVAYGDYIYFFFREIAV 225
Qy 242 EYNTMGKVVFPRAQVCKNDMGGSSQRVLEKQWTSFLKARLNCSVPGDSHFYFNILQAVTD 301
Db 226 EYMNCGKVIYSRVARVCKDDKGPHQSRRDR-WTSFLKARLNCSIPGEYPFYFDEIQSTSD 284
Qy 302 VI--RINGRD---VVLATFSTPYNSIPGSACVAYDMLDIASVFTGRFKEQKSPDSTWTPV 356
Db 285 IVEGRYNSDDSKKIYGLITTPVNAIGGSAICAYQMADILRVFEGSFKHQETINSNWLPV 344
Qy 357 PDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMV 416
Db 345 PQNLVPEPRPGQCVRDSRI-----LPDKNVNFIKTHSLMED-VPALFGKPVLRVSL 395
Qy 417 RYRLTKIAVDTAAGPYQNH--TVVFLGSEKGIILKFLARIGNSGFLNDSLFLLEMSVYNS 474
Db 396 QYRFTAITVDPQVKTINNQYLDVLYIGTDDGKVLK----- 430
Qy 475 EKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCV-----IKVP----- 511
Db 431 -----AVNIPKRHAKALLYRKYRTSVPHGAPVKQLKIAPIGYGVVVVGKDEI 478
Qy 512 ---LGRCERHGKCKTCIASRDPYCGWIKEGGACSHLSPNSRLTF-EQDIERGN---- 561
Db 479 RIANLNHCASKTRC-KDCVELQDPHCAWDQNLCSVIDTVTSYRFLIQDVVRGDDNKCW 537
Qy 562 ---TDGLGDCHNSFVALNGHSSLLPSTTSSTAQEGYESRGGMLDWKHLLDSPDSTDPM 618
Db 538 SPQTDKKTVIKNK-----PSEVENEIT-----NSIDEKDL---DSSDP 572
Qy 619 LGAVSSHQDKKGVIRESYLGK-HDQLVPVT--LLAIAVILAFVMGA--VFSGITV 670
Db 573 LIKTGLDDSDCDPV-SENSIGGCAVRQLVIYTAGTLHIVVVVVSVIVGLFSWLYSGLSV 631
Qy 671 YCV--CDHRRKDVAVVQRKE--KELTHSRRGSMS-SVTKLSGLFGDTQSKDPKPEAILTP 725
Db 632 FAKFHSDSQYPEAEIFEQHNHLERLSANQTYLTPRANKAVNLVVKVSSSTPRPKKDNL 691
Qy 726 LMHNGKLATPGNTAKM 741
Db 692 VSKDNLNIAASDGTLOKI 707

RESULT 15
SZ1B BRARE

ID SZ1B_BRARE STANDARD; PRT; 778 AA.

AC Q9W686;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Semaphorin Z1B precursor (Semaphorin 1B) (Sema-Z1B).

GN SEMAZ1B OR SEMA3AB.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99425174; PubMed=10495275;

RA Roos M., Schachner M., Bernhardt R.R.;

RT "Zebrafish semaphorin Z1b inhibits growing motor axons in vivo.";

RL Mech. Dev. 87:103-117(1999).

CC -!- FUNCTION: MIGHT NORMALLY INFLUENCE THE MIDSEGMENTAL PATHWAY CHOICE
OF THE VENTRALLY EXTENDING MOTOR AXONS BY CONTRIBUTING TO A
REPULSIVE DOMAIN IN THE POSTERIOR SOMITE.

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- TISSUE SPECIFICITY: EXPRESSED IN RHOMBOMERES THREE AND FIVE, AND
IN THE POSTERIOR HALF OF NEWLY FORMED SOMITES WHICH IS AVOIDED BY
VENTRALLY EXTENDING MOTOR AXONS.

CC -!- SIMILARITY: Belongs to the semaphorin family.

CC -!- SIMILARITY: Contains 1 Sema domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -----

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CC -----

DR EMBL; AF083382; AAD28103.1; -.

DR ZFIN; ZDB-GENE-991209-6; sema3ab.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003659; Plexin-like.

DR InterPro; IPR002165; Plexin_repeat.

DR InterPro; IPR001627; Sema.

DR Pfam; PF00047; ig; 1.

DR Pfam; PF01437; PSI; 1.

DR Pfam; PF01403; Sema; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00423; PSI; 1.

DR SMART; SM00630; Sema; 1.

DR PROSITE; PS50835; IG LIKE; 1.

KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;

KW Developmental protein; Glycoprotein.

FT SIGNAL 1 17 POTENTIAL.

FT CHAIN 18 778 SEMAPHORIN Z1B.

FT DOMAIN 241 539 SEMA.

FT DOMAIN 579 668 IG-LIKE C2-TYPE.

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